

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 181255

TO: Ruixiang Li

Location: REM-4D59/4C70

Art Unit: 1646

March 14 2006

Case Serial Number: 10/782596

From: P. Sheppard

**Location: Remsen Building** 

Phone: (571) 272-2529

sheppard@uspto.gov

| Search Notes |     | · · |   |
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### STIC-Biotech/ChemLib

Please do a standard search on:

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To: Subject: Li, Ruixiang

Saturday, March 04, 2006 9:34 AM

Sequence search of Application No.10/782,596

STIC-Biotech/ChemLib

181255

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Vendors and cost where applicable

STN:\_

DIALOG:

QUESTEL/ORBIT:

WWW/Internet:\_ Other (Specify):\_

SEQUENCE SYSTEM:

LEXIS/NEXIS:

| (i). SEQ ID NO: 20 against amino a                                     | cid databases (excluding pending databases). |  |
|--|--|--|
| Thank you very much!   |  |  |
| Ruixiang Li<br>GAU 1646<br>REM 4D59<br>Mail Box 4C70<br>(571) 272-0875 |  |  |
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\_ AA#:\_

\_Text:\_

\_\_ Litigation:\_\_

\_\_Oligomer:

Encode/Transl:\_

Structure #:\_

Inventor:\_\_\_

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| 1 1 3 4 5 7 7 1 1 3 4 5 7 7 1 1 3 4 5 7 7 1 1 3 4 5 7 7 1 | 1986<br>1986<br>1975<br>1975 |      | Length 373 373 373 373 373 | B   144414                                    | UMAN<br>HUMAN<br>BOVI<br>OUSE<br>AT | Description Q9ns66 homo sapien Q5hyq4 homo sapien Q5e9h8 bos taurus Q6pi62 mus musculu Q9jjh2 rattus norv O4va66 mus muscus |
|---|------------------------------|------|----------------------------|---|-------------------------------------|---|
| ı ov or   |                              | 99.1 | 373<br>373                 | , D L   | GP173 RAT<br>Q4VA66 MOUSE           |   |
| es ~1   | 1625.5<br>1464               |      | 387<br>349                 |   | GP173_BRARE<br>Q4S5Y6_TETNG         | Q9i918 brachydanio<br>Q485y6 tetraodon n  |
| ωa  | 1344                         | 67.5 | 328                        | N 1   | Q4T258 TETNG                        | Q4t258 tetraodon  |
| 10  | 1291.5                       | 64.8 | 370                        |   | Q5U576 XENLA                        | ×   |
| 11  | 1291.5                       |      | 371                        |   | Q4RHK7_TETNG                        |   |
| 12  | N                            |      | 370                        |   | GPR85_HUMAN                         |   |
| 13  | 1288.5                       | 64.7 | 370                        | ۲   | GPR85_MOUSE                         | P60894 mus musculu  |
| 14  | 1288.5                       | 64.7 | 370                        | <u>سر</u>                                     | GPR85_RAT                           | P60895 rattus norv  |
| 15  | 1288.5                       | 64.7 | 370                        | N   | Q8NEN2_HUMAN                        |   |
| 16  | N                            | ٠    | 370                        | N   | Q6ZWR2_MOUSE                        |   |
| 17  | 1288.5                       | 64.7 | 371                        | _   | GPR85_BRARE                         | Q9i919 brachydanio  |
| 18  | N                            | •    | 370                        | N   | Q5RBG7_PONPY                        | Q5rbg7 pong   |
| 19  | 1129                         | 56.7 | 292                        | 2   | Q4SR11_TETNG                        | Q4srll tetraodon n  |
| 20  | 1031                         | •    | 375                        | Ц   |                                     | Q9ns67 homo sapien  |
| 21  | 1023                         | 51.4 | 377                        | <u>, , , , , , , , , , , , , , , , , , , </u> | GPR27_RAT                           |   |
| 22  | 1022                         | •    | 379                        | بر  | GPR27_MOUSE                         | mus   |
| 23  | 963                          | •    | 187                        | N   | Q80T44 MOUSE                        | Q80t44 mus musculu  |
| 24  | 583                          | •    | 281                        | N   | Q4R8W0_MACFA                        |   |
| 25  | 275                          | •    | 357                        | N   | Q6TLJ0_MUSPF                        | Q6tlj0 mustela pu   |
| 26  | 274                          | 13.8 | 501                        | N   | Q4T4F3_TETNG                        | Q4t4f3 tetraodon  |
| 27  | 270.5                        | •    | 456                        | N   | Q8TOY4_APIME                        | Q8t0y4 apis mellif  |
| 28  | 269.5                        | •    | 470                        | μ.  | 5HT2A PIG                           | P50129 sus  |
| 29  | 267.5                        | 13.4 | 470                        | ب   | SHT2A BOVIN                         | Q75z89 bos  |
| 30  | 266.5                        | 13.4 | 470                        | _   | SHT2A CANFA                         | 046635 canis  |
| u<br>H  | 266.5                        | 13.4 | 470                        | N   | Q50DZ9 CANFA                        | 9   |
|   | -                            |      |                            |   | •                                   |   |

| 264 13.3 389 7 1 DKU9 MOUSE 264 13.3 389 7 2 QRTES MOUSE 261.5 13.1 387 2 QSBXS4 MOUSE 261.5 13.1 387 2 QSBXS4 MOUSE 261 13.1 382 2 QSDJ14 BRARE 261 13.1 400 1 DRD3 HUMAN 260 13.1 400 1 DRD3 HUMAN 260 13.1 400 2 Q4VBM8 HUMAN 259.5 13.0 471 1 SHT2A CRIGR 259.5 13.0 471 1 SHT2A MACMU 259.5 13.0 471 1 SHT2A MACMU 259.5 13.0 471 1 SHT2A MACMU 259.5 13.0 471 1 SHT2A RAT 259.5 13.0 471 1 SHT2A RAT 259.5 13.0 471 2 QS43D4 MOUSE 259.5 13.0 471 2 QS43D4 MOUSE 259.5 13.0 471 2 QS43D4 MACFA 259.5 13.0 471 1 SHT2A RAT 259.5 13.0 471 1 SHT2A RAT 259.5 13.0 471 1 SHT2A HUMAN | 45          | 44           | 43           | 42          | 41          | 40          | 9           | 38            | 37          | 36          | 35           | 34           | ω<br>ω       | 3.2        |
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| 387 2<br>387 2<br>382 2<br>400 1<br>400 2<br>471 1<br>471 1<br>471 1<br>471 2<br>473 2  | 257         | 258          | 259.5        | 259.5       | 259.5       | 259.5       | 259.5       | 260           | 260         | 261         | 261          | 261.5        | 264          | 254        |
| 1001111011001   | 12.9        | 13.0         | 13.0         | 13.0        | 13.0        | 13.0        | 13.0        | 13.1          | 13.1        | 13.1        | 13.1         | 13.1         | 13.3         | 13.3       |
| 2 Q7TT80 MOUSE 2 Q8BXS4 MOUSE 2 Q8BXS4 MOUSE 2 Q8BXS4 MOUSE 2 Q5DJ14 BRARE 1 DRD3 PANTR 1 DRD3 HUMAN 2 Q4VBM8 HUMAN 2 Q4VBM8 HUMAN 3 CATCAR 1 SHT2A MOUSE 1 SHT2A RAT 2 G543D4 MOUSE 2 Q51SK8 MACFA 1 SHT2A HUMAN 1 SHT2A HUMAN   | 471         | 439          | 471          | 471         | 471         | 471         | 471         | 400           | 400         | 400         | 382          | 387          | 389          | 186        |
| DRU9 MOUSE Q7TT80 MOUSE Q8BXS4 MOUSE Q5DJ14 BRARE DRD3 PAWR DRD3 HUMAN Q4VBM8 HUMAN Q4VBM8 HUMAN Q4VBM8 HUMAN G5HT2A MACMU GHT2A MOUSE SHT2A RAT G543D4 MOUSE Q543D4 MOUSE  | ٠,          | N            | N            | μ           | _           | _           | ۰           | N             | سا          | بر          | N            | Ŋ            | N            | ۲          |
|   | 5HT2A HUMAN | Q5ISK8_MACFA | Q543D4_MOUSE | SHT2A_RAT   | 5HT2A_MOUSE | 5HT2A_MACMU | 5HT2A_CRIGR | Q4 VBM8_HUMAN | DRD3_HUMAN  | DRD3_PANTR  | Q5DJ14_BRARE | Q8BXS4_MOUSE | Q7TT80_MOUSE | DRU4 MOUSE |
|   | homo sapien | macaca fasc  | mus musculu  | rattus norv | mus musculv | macaca mula | cricetulus  | homo sapier   | homo sapier | pan troglod | brachydanic  | mus musculu  | mus musculu  | muscutu    |

## ALIGNMENTS

|   | R R R R R R R R R R R R R R R R R R R   | GP173 J<br>ID GGP173 J<br>AC QU<br>DT 11<br>DT 11<br>DT 11<br>DT 11<br>DT 11<br>OS H<br>OC M  |
|---|---|---|
| Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDMA sequences."; proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  -!- FUNCTION: Orphan receptor!- SUBCELIULAR LOCATION: Integral membrane protein (By similarity)!- TISSUB SPECIFICITY: Expressed at high levels in brain and ovary. Lower levels in small intestine. In brain regions, detected in all regions tested. Highest levels in the cerebellum and cerebral | QUENCE.  QUENCE.  QUENCE.  DOI=10.1006/bbrc.2000.2829; Saito T., Takasaki J., Kamohara M., Sugimoto T., Saito T., Takasaki J., Kamohara M., Sugimoto T., Tadokoro M., Matsumoto S., Ohishi T., Furuichi K., SR  Tadokoro M., Matsumoto S., Ohishi T., Furuichi K., Taeberg L.A., Grouse L.H., Derge J.G., Colling F.S., Wagner L., Schaefer C.F., Bhat N.K., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Marusina K., Farmer A.A., Rubin G.M., Hong L., | ULT 1 GP173 HUMAN STANDARD; PRT; 373 AA. GP173 HUMAN STANDARD; PRT; 373 AA. Q9NS6; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2005 (Rel. 40, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) Probable G-protein coupled receptor 173 (Super conserved receptor expressed in brain 3). Name=GPR173; Synonyms=SREB3; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; |

SIMILARITY:

Belongs to the G-protein coupled receptor 1 family.

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Query Match
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Matches 372
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GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PP00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODDPSN.
PROSITE; PR00237; GPCRRHODDPSN.
PROSITE; PS00237; GPCRHEIN RECEP F1 1; FALSE_NEG.
PROSITE; PS00237; GPROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Glycoprotein; Multigene family; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB040801;
EMBL; BC009861;
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Ensembl; ENSG00000184194;
HGNC; HGNC:18186; GPR173.
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                                                                                                                                                                                                              LLDLCLADGIRSAVCFPFVLASVRHGSSWTFSALSCKIVAFMAVLFCFHAAFMLFCISVT
                                    PYIVACYWRVFVKACAVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLKKCLTTHAPCWGT
                                                                                                                                FKANDTIGFMIMLAVIMAATHAVYGKILILFEYRHRKMKPVQMVPAISQNWTFHGPGATGQ
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GGAPAPREPYCVM 373
                                                                      AAANWIAGFGRGPMPPTLLGIRQNGHAASRRLLGMDEVKGEKQLGRMFYAITLLFLLLWS
                                                                                                                   FKANDTLGFMLMLAVLMAATHAVYGKLLLFEYRHRKMKPVQMVPAISQNWTFHGPGATGQ
                        PYIVACYWRVFVKACAVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLKKCLRTHAPCWGT
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llarity 99.7%;
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AAH09861.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                           MW.
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                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic (Potential).
N-linked (GlcNAc. . .) (Pot
N-linked (GlcNAc. . .) (Pot
N-linked (GlcNAc. . .) (Pot
By similarity.
By 8A227F914C9D8358 CRC64;
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Pred. No. 1.9e-145;
0; Mismatches 1;
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Extracellular (Potential)
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RESULT 3
Q5E9H8 BOVIN
ID Q5E9H8;
AC Q5E9H8;
DT 10-MAY-2005 (TrEMBLrel.

PRELIMINARY;

PRT;

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RESULT 2
OSHYQ4 HUMAN
OSHYQ4;
ID OSTYQ4_HUMAN PRELIMINARY;
AC QSHYQ4;
DT 10-MAY-2005 (TrEMBLrel. 30,
DT 10-MAY-2005 (FROME)
GO ENARYOTA; Butheria; Euarchol
OC Mammalia; Eutheria; Euarchol
OC Mammalia; Eutheria; Euarchol
OC Mammalia; Eutheria; Euarchol
OC HOMO.
OX NCBL_TAXID=9606;
RN NUCLEOTIDE SEQUENCE.
RA HOWden P.;
RP NUCLEOTIDE SEQUENCE.
RA HOWden P.;
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Best Local S
Matches 372
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EMBL; BX32835; CAI42530.1; -; Genomic DNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001284; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; I
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCREHODOPSN.
PRINTS; PR00237; GPCREHODOPSN.
ROSITB; PS02062; GPROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SEQUENCE 373 AA; 41481 MW; 8A227F914C9D8358 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    i0-MĀY-2005 (TrEMBLrel. 30, Created)
10-MĀY-2005 (TrEMBLrel. 30, Last sequence update)
10-MĀY-2005 (TrEMBLrel. 30, Last annotation update)
10-MĀY-2005 (TrEMBLrel. 30, Last annotation update)
G-protein coupled receptor 173.
Name=GPR173; ORFNames=RP1-290F12.1-001;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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                                         GGAPAPREPYCVM
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   GGAPAPREPYCVM
                                                                                                                        PYIVACYWRVFVKACAVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLKKCLRTHAPCWGT
                                                                                                                                                           PYIVACYWRVFVKACAVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLKKCLTTHAPCWGT
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Best Local S
Matches 370
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R EMBL; BT020942; AAX08959.1; -; mRNA.

R G0; G0:0016021; C:integral to membrane; IEA.

R G0; G0:0004872; F:receptor activity; IEA.

R G0; G0:0001584; F:rhodopsin-like receptor activity; IEA.

R G0; G0:0007186; P:G-protein coupled receptor protein signalin. .;

R G0; G0:0007165; P:signal transduction; IEA.

R InterPro; IPR000276; GPCR_Rhodpsn.

R F1NTS; PR00237; GPCR_Rhodpsn.

R PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

R PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Receptor; Transducer; Transmembrane.

G-protein coupled receptor; Receptor; Transducer; Transmembrane.
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Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
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Harhay G.P., Sonstegard T.S.,
Snelling W.M., Weidmann R.T.,
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Mammalia; Eutheria; Lauraa
Pecora; Bovidae; Bovinae;
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GGAPAPREPYCVM
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(TrEMBLrel. 30, Last annotation update)
pupled receptor 173.
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Smith T.P.L.;
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human
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25-OCT-2004 (Rel. 45, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Probable G-protein coupled receptor 173 (Super conserved receptor expressed in brain 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
Muroidea;
                                                                                                                                                                                                                                                                                                                                  PRIMTS; PR00237; GPCRHIODOBSN.
PROSITE; PS00237; G-PROTEIN RECEP F1_2;
PROSITE; PS50262; G-PROTEIN RECEP F1_2;
G-protein coupled receptor; Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proc. Natl. Acad. Sci. U.S.
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                Transducer;
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InterPro; IPR000276; GPCR_Rhodpsn.
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European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Orphan receptor.
SUBCELLULAR LOCATION: Integral membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC043021; AAH43021.1; -; MGI:1918021; Gpr173.
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GP173_RAT
Q9JJH2;
16-OCT-2001
                                                                         MEDLINE=20294882; PubMed=10833454; DOI=10.1006/bbrc.2000.2829; Matsumoto M., Saito T., Takasaki J., Kamohara M., Sugimoto T., Kobayashi M., Tadokoro M., Matsumoto S., Ohishi T., Furuichi K., Kobayashi M., Tadokoro M., Matsumoto S., Ohishi T., Furuichi K., "An evolutionarily conserved G-protein coupled receptor family, sexpressed in the central nervous system."; expressed in the central nervous system."; eliophys. Res. Commun. 272:576-582(2000).
-I-FUNCTION: Orphan receptor.
-I-SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Probable G-protein coupled receptor 173 (Super expressed in brain 3)
Name=Gpr173; Synonyms=Sreb3;
Rattus norvegicus (Rat)
            This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                               RACCUB NOTVEGICUS (RAT).

EUKATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
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TISSUE=Brain;
                                                SUBCELLULAR LOCATION: Integral membrane protein (By similarity). SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
ween the Swiss Institute of Bioinformatics Institute. European Bioinformatics Institute. as long as its content is in no way
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RESULT 6

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Q4VA66, MOUSE PRELIMINARY; PRT; 373 AA.

AC Q4VA66;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Super conserved receptor expressed in brain 3.

GN Name=Gpr173;
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A Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altechul S.F., Zeeberg B., Buctow K.H., Schenfer C.F., Bhat N.K.,
A Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bonak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Schnernch A., Schein J.E., Jones S.J.M., Marra M.A.;
Tand mouse cDNA sequences ",
Tand mouse cDNA sequences ",
Tand mouse cDNA sequences ",
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Best Local S
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MGI; MGI; JER000276; GFCR_Rhodpsn.

InterPro; JER000276; GFCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.

PR.NTS; PR00237; GFCRRHODDPSN.

PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.

G-protein coupled receptor; Receptor; Transducer; SEQUENCE 373 AA; 41511 MW; C06DEA2F0E8BCAF5 CR
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STRAIN=C57BL/6; TISSUE=Mouse;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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Submitted (MAY-2
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                                                                                       | PYIVACYWRVFVKACAVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLKKCLTTHAPCWGT
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GGAPAPREPYCVM 373
                                                      PYTVACYWRVFVKACAVPHRYLATAVWMSFAQAAVNPTVCFLLNKDLKKCLRTHAPCWGT
                                                                                                                                                                        AAANWIAGFGRGPMPPTLLGIRQNGHAASRRLLGMDEVKGEKQLGRMFYAITLLFLLLWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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99.2%;
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1; Mismatches
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Pred. No. 1
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PROSITE; PS00237; GFROTEIN_RECEP_F1_1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=gpr173; Synonyms=sreb3;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-MAY-2005 (Rel. 47, Last annotation update)
Probable G-protein coupled receptor 173 (Super expressed in brain 3).
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Q91918;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matsumoto M., Saito T., Takasaki J., Kamohara M., Sugimoto T. Kobayashi M., Tadokoro M., Matsumoto S., Ohishi T., Furuichi "An evolutionarily conserved G-protein coupled receptor famile processed in the central nervous system.";
                                                                                                                                                                                                                                                                                                               G-protein coupled receptor; Glycoprotein; Multigene family; Receptor;
                                                                                                                                                                                                                                                                                                                                                                             ZFIN; ZDB-GENE-000710-1; gpr173.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB040806; BAA96652.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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MEDLINE=20294882; Pu
                                                                                                                                                                                                                                                              MOD OGOL
                                                                                                                                                                                                                                                                                                   Transducer;
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             Similarity
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Conservative
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 25;
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1 (Potential).

Cytoplasmic (Potential).

2 (Potential).

2 (Potential).

5 (Potential).

Cytoplasmic (Potential).

4 (Potential).

6 (Potential).

5 (Potential).

6 (Potential).

Cytoplasmic (Potential).

6 (Potential).

Cytoplasmic (Potential).

6 (Potential).
Score 1625.5;
Pred. No. 1.5e
25; Mismatches
                                                Cytoplasmic (Potential).

-linked (GLCNAc. . ) (Potential).

N-linked (GLCNAc. . ) (Potential).

By similarity.

5E094EFD44120871 CRC64;
                                                                                                                   Extracellular (Potential).
7 (Potential).
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            1625.5; DB 1
No. 1.5e-117;
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                            387;
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*RESULT OF REAL MANAGEMENT OF RE
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A Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

A Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

A Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

A Anthouard V., Jubin C., Castelli V., Boudet N., Castellano S.,

A Anthouard V., Jubin C., Castelli V., Poulain J., De Herardinis V.,

A Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

A Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

A Cruaud C., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

A Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

A Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

A Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals

"The early vertebrate proto-karyotype.";

L. Nature 431:946-957(2004).
preliminary data.

EMBL; CAAEG1014729; CAG03946.1; -; Genomic_DNA.

InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.

PRNITS; PR00237; GPCRRHODDPSN.
PROSITE; PS50262; G_PCOTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transducer;
NON_TER
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13-SEP-2005
13-SEP-2005
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
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Submitted (FEB-2004) to
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EMBL/GenBank/DDBJ whole
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                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.

A Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

A Mauceli E., Bouneau L., Fischer S., Lutfalla G., Dossat C., Segurens B.,

A Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

A Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

A Anthouard V., Jubin C., Castelli V., Fatinka M., Vacherie B.,

A Hiemont C., Salanoubat M., Levy M., Poulain J., De Berardinis V.,

Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

Cruaud C., Lardier S., Brottier P., Coutanceau J.P., Gouzy J.,

A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

A Findblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Liudblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

A Liudblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals

"The early vertebrate proto-karyotype.";

L., Nature 431:946-957(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tetraodon nigroviridis (Green puffer).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                NUCLEOTIDE SEQUENCE.
Genoscope; Whitehead Ins
Submitted (FEB-2004) to
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                           preliminary data.
EMBL; CAAE01010335; C
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. 31, Last annotation
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Last annotation update)
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Pred. No. 4.2e
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                             Genomic_DNA
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Best Local S
Matches 257
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G-protein
NON_TER
MEDLINE-2398257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausmer R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz
                                                                                                Dev.
                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; l
Amphibla; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                      01-FEB-2005
LOC495345 pr
                                                                                                                                                                                                                                                                                                                 Q5U576_XENLA
Q5U576;
                                                                                                                                                                                                                                                          LOC495345 protein.
Name=LOC495345;
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PRINTS; PR00237; GFCRRHODOPSN.

PROSITE; PS50262; G PROTEIN RECEP F1_2;

G-protein coupled receptor; Receptor; Tr
                                                                                                                                          Richardson
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                                                                             TISSUE-Eye
                                                                                      NUCLEOTIDE
                                                                                                                      initiative
                                                                                                                                                  Klein S.L.,
                                                                                                                                                             MEDLINE=22341132; PubMed=12454917;
                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                       NCBI_TaxID=8355;
                                                                                                                              "Genetic
                                                                                                                                                                                                                                                                                                                                      XENLA
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                                                                                                                        and genomic ve.":
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(TrEMBLrel.
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68.7%;
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Pred. No. 7.5e
31; Mismatches
                                                                                                                                                    Wagner
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                                                                                                                              Xenopus
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annotation
                                                                                                                                                  DOI=10.1002/dvdy.10174;
r L., Pontius J., Clifton
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RESULT 11
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ID Q4RK7;
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Best Local S
Matches 234
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PRINTS; PR00237; GFCRHODOPSN.
PROSITE; PS50262; G PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transducer; SEQUENCE 370 AA; 41904 MW; 8A459AD950886FF3 CR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Integral membrane protein EMBL, BC084808; AAH84808.1; -; mRNA. GC; GC:0016021; C:integral to membrane; IEA. GC; GC:0004872; F:receptor activity; IEA. GC; GC:0001584; F:rhodopsin-like receptor activity; GC; GC:0007186; P:G-protein coupled receptor protein GC; GC:0007186; P:G-protein coupled receptor brotein GC; GC:0007186; P:G-protein coupled receptor protein GC; GC:0007186; P:G-protein coupled receptor protein GC; GC:0007186; P:G-protein coupled receptor brotein GC; GC:0007186; P:G-protein GC:0007186; P:G-protein
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TION: Integral membrane pr
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                                                                                                                                                                                                                                                                                         373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1291.5;
Pred. No. 9.7e
58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99:16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370;
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(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

31, 31,

Created)
Last sequence update)
Last annotation update)

PRELIMINARY;

371 ₽

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RESULT 12
GPR85_HUMAN
ID GPR85_HUMAN
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RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Micaud S., Jaffe D., Fishers S., Lutfalla G., Dossat C., Segurens B.,
RA Micaud S., Jaffe D., Fishers S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Crusud C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Crusud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Crusud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Rallis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA Kindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
The early vertebrate proto-karyotype.";
Nature 431:946-957 (2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50262; G PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transducer;
SEQUENCE 371 AA; 41990 MW; ACE9C71638B153E5 CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetraodon nigroviridis (Green puffer).

Bukaryota; Metazoa; Chordata; Cranitata; Vertebrata; Euteleostom
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleost
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORFNames=GSTENG00034295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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Pfam; PF00001: 7tm 1. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary data.
SUBCELLULAR LOCATION: Integral
C; CAAE01015045; CAG12125.1; -;
                                                                                                                                                          320
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                                                                                                                                                                                                                                                                                                                 HAVYGKILLFEYRHRKMKPVQMVPAISQNWTFHGPGATGQAAANWIAGPGRGPMPPTLLG
                                                                                                                                                                                                                                                                                                                                                                                                  AAVICWAWTLSVAMAFPPVFDVGTYKFIRBEDQCIFBHRYFKANDTLGFMLMLAVLMAAT
                                                                                                                                                            RYLATAVWMSFAQAAVNPIVCFLLNKDLKKCL-TTHAPCWGTGGAPAPREPYCVM
                                                                                                                                                                                                                                                                                                                                                                          LAVICMVWTLSVAMAFPPVLDVGTYSFIREEDQCTFQHRSFRANDSLGFMLLLALILLAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASVRHGSSWTFSALSCKIVAFMAVLFCFHAAFMLFCISVTRYMAIAHHRFYAKRMTLWTC
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                                                                                                                     GYLTAAVWMSFAQAGVNPFICIFSNRELRRCFSTTLLYC-
                                                                                                                                                                                                                                            IRONGHAAS-RRLLGMDEVKGEKOLGRMFYAITLLFLLLWSPYIVACYWRVFVKACAVPH
                                                                                                                                                                                                                                                                                        QLVYLKLIFFVHDRRKMKPVQFVPAVSQNWTFHGPGASGQAAANWLAGFGRGPTPPTLLG
                                                                                                                                                                                                    IRQNSNAAGRRRLLVLDEFKTEKRISRMFYIMTFFFLALWGPYLVACYWRVFARGPVVPG
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             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1291.5; DB 2;
Pred. No. 9.7e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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             370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane.
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                 Biochim.
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RX MEDLINES 2247399; Pubmede112853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wajner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wylle K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Wylle K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Karkins R., Strommatt C.,
RA Califeri L., Holmes R., Minx P., Maupin R., Strommatt C.,
RA Hickenbotham M.T., Eddred J., Williams D., Bedell J.A., Spieth J.,
RA Hickenbotham M.T., Chisses S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadanoto S., Bubb K.,
RA Simms E., Levy R., Clendemning J., Kault R., Kent W.J., Furey T.S.,
RA Baertsch R.A., Brent M.R., Kebler B., Flicek P., Bork P., Suyama M.,
Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Marerero P. H. Wilson R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                         Eddy S.R., McPherson אייי ביינו
Waterston R.H., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hellebrand S., Schaller H.C., Wittenberger T.; "The brain-specific G-protein coupled receptor GPR85 with identical protein sequence in man and mouse maps to human chromosome 7q31.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probable G-protein coupled expressed in brain 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P60893; Q9JHI6; Q9NPD1;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation updat
                                                                                                                                                                       "The DNA sequence of human Nature 424:157-164(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suwa M., Sato T., Okouchi I
Tsutsumi S., Aburatani H.,
"Genome-wide discovery and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
Suwa M., Sato T., O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "An evolutionarily conserved G-pa
expressed in the central nervous
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Kobayashi M., Tadokoro M., Matsumoto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=GPR85; Synonyms=SREB2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rissue=Amygdala;
FUNCTION: Orphan receptor.

FUNCTION: Orphan receptor.

SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

TISSUB SPECIFICITY: Highly expressed in brain and testis. Lower

TISSUB SPECIFICITY: Highly expressed in brain and testis. Tower

levels in small intestine, placenta and spleen. In brain regions,

levels in small regions tested, but somewhat lower levels in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence in man and mouse maps to human Biophys. Acta 1493:269-272 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biophys.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JUL-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Okouchi I., Arita M., Futa
atani H., Asai K., Akiyama
overy and analysis of human
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272:576-582(2000)
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-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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PRINTS; PRO0237; GECRENDEDESN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Glycoprotein; Multigene family; Receptor;
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L; AL161959; CAB8
L; AC073346; AAQ9
; T47131; T47131.
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                                SPYIVACYWRVFVKACAVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLKKCL-TTHAPCW
                                                                                                                                                                                                                                 RYLAIAHHRFYTKRLTFWTCLAVICMVWTLSVAMAFPPVLDVGTYSFIRBEDQCTFQHRS
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GPYLVACYWRVFARGPVVPGGFLTAAVWMSFAQAGINPFVCIFSNRELRRCFSTTLLYC-
                                                                                                 AAANWIAGFGRGPMPPTLLGIRQNGHAAS-RRLLGMDEVKGEKQLGRMFYAITLLFLLLW
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                                                                           AAANWLAGFGRGPTPPTLLGIRQNANTTGRRRLLVLDEFKMEKRISRMFYIMTFLFLTLW
                                                                                                                                                      FRANDSLGFMLLLALILLATQLVYLKLIFFVHDRRKMKPVQFVAAVSQNWTFHGPGASGQ
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Bioinformatics
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N-linked (GlcNAc. . .) (Potential).

N-linked (GlcNAc. . .) (Potential).

N-linked (GlcNAc. . .) (Potential).
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4 (Potential).
Extracellular (Potential)
5 (Potential)
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Pred. No. 1.7e-91;
6; Mismatches 77
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RESULT
GPR85_M
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RM MEDININE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RN MEDININE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.M., Wallalon A., Young A.C.,
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MEDLINE=2043531; PubMed=10978537; DOI=10.1016/S0167-4781(00)00182-;
MEDLINE=2043531; PubMed=10978537; DOI=10.1016/S0167-4781(00)00182-;
Hellebrand S., Schaller H.C., Wittenberger T.;
"The brain-specific G-protein coupled receptor GPR85 with identical protein sequence in man and mouse maps to human chromosome 7q31.";
                                                                                                                                                                                                            EMBL; AF254416; AAF79959.1; -; EMBL; BC026975; AAH26975.1; -; EMBL; BC065154; AAH65154.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Orphan receptor.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity)
-!- TISSUE SPECIFICITY: Exclusively expressed in brain.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Muroidea; Muridae; Murinae; Mus.
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Name=Gpr85; Synonyms=Sreb2;
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P60894; Q9UHI6; Q9NPD1;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                           MGI; MGI:1927851; Gpr85.
GO; GO:0016021; C:integral to membrane;
InterPro; IPR000276; GPCR Rhodpsn.
                                                                                                                                                                         Ensembl; ENSMUSG00000048216; Mus musculus.
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mRNA.
mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                              way modified
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PROSITE; PS50262; (
G-protein coupled ;
Transducer; Transme
TOPO DOM 1
TRANSMEM 26
TOPO DOM 47
TRANSMEM 58
TOPO DOM 79
TRANSMEM 79
TRANSMEM 97
TRANSMEM 97
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DISULFID
SEQUENCE
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TRANSMEM
TOPO DOM
TRANSMEM
                Name=Gpr85; Synonyms=Sreb2;
Rattus norvegicus (Ratl).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodent
Muroidea; Muridae; Murinae; Rattus.
                                                                                                     GPR85 RAT STANDARD; PRT; 37
P60895; Q9JHI6; Q9NPD1;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence upd
10-MAY-2005 (Rel. 47, Last annotation u
Probable G-protein coupled receptor 85
expressed in brain 2) (PKTCX1).
 Muroidea; Muridae
NCBI_TaxID=10116;
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RAT
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                                                                                                                                                                                                                                                                                                                                       GTGGAPAPREPYCVM
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209 209
310 286
313 313
4 334
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3182
1722 MW;
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G_PROTEIN_RECEP_F1_2; 1.
receptor; Glycoprotein; Multigene family; Receptor;
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62.7%;
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Extracellular (Potential).
3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
5 (Potential).
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7 (Potential).
Cytoplasmic (Potential).
N-linked (GLONAc. .) (Potential).
N-linked (GLONAc. .) (Potential).
N-linked (GLONAc. .) (Potential).
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Pred. No. 1.7e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              By similarity.
7B67A39F6166AAEB CRC64;
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2 (Potentia
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                                                                                                                             update)
|5 (Super
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nes 77;
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                                      Rodentia;
                                                                                                                             conserved
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                                                       Euteleostomi;
                                    Sciurognathi;
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Eiochem. Biophys. Res. Commun. 272:576-582 (2000).
                                                                                                                                                                                  TOPO DOM
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                        TOPO DOM
TRANSMEM
TOPO DOM
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MEDLINE=20794882; PubMed=10833454; DOI=10.1006/bbrc.2000.2829;
Matsumoto M., Saito T., Takasaki J., Kamohara M., Sugimoto T.,
Matsumoto M., Saito T., Takasaki J., Cariohi T., Furnichi K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
                                                                                                                                                           CARBOHYD
DISULFID
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Submitted (DEC-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley;
Kim H., Park S., Kang Y., Kim C., Jeon J.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                             TOPO DOM
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                                                                                                                                                                                                                                                                                                                                                                                                         prosite; ps00237; G protein_recep_r1_1; FALSE_NEG.
prosite; ps50262; G_protein_recep_r1_2; 1.
G-protein coupled receptor; Glycoprotein; Multigene family; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB040803; BAA96649.1; -; EMBL; AF203907; AAG42284.1; -; EMBL; BC087727; AAH87727.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: Orphan receptor.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                    TOPO
                                                                                                                                                                                                                                                                                                                                                                                Transducer;
TOPO_DOM
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ensembl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
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 59
                        61
                                                                        μ
                                                 Н
                                                                                                             Similarity
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LLDLCLADGIRSAVCEPEVLASVRHGSSWTESALSCKIVAFMAVLECEHJAEMLECISVT
                                               MANTTGEPEEVSGALSPPSASAYVKLVLLGLIMCVSLAGNAILSLLVLKERALHKAPYYF
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                                                                                                 Conservative
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                                                                                                             64.7%;
62.7%;
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                                                                                                                                             1 (Potential).
Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential).
3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
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5 (Potential).
6 (Potential).
6 (Potential).
7 (Potential).
Extracellular (Potential).
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Cytoplasmic (Potential).
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                                                                                                 56;
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausmer R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schuntz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schuntz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schuntz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
"Generation and initial analysis of more than 15,000 full-length human
   GO; GO: 00
GO; GO: 00
GO; GO: 00
GO; GO: 00
Interpro;
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NUCLEOTIDE
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                                                                                                                                                     Submitted
                                                                                                                                                                  Strausberg
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Eukaryota; Metazoa; Chordata; Craniata
Mammalia; Eutheria; Euarchontoglires;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBNEN2 HUMAN
QBNEN2;
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                                                                                                                                                                                     TISSUE-Testis;
mitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. SUBCELLULAR LOCATION: Integral membrane protein (By SIL; BC030577; AAH30577.1; -; RNAB. GO:0016021; C:integral to membrane; IEA. GO:0004872; F:receptor activity; IEA. GO:0001584; F:rhodopsin-like receptor activity; IEA. GO:0007165; P:groretin coupled receptor protein sig GO:0007165; P:signal transduction; IEA.
                                                                                                                                                                                                                                          ouse cDNA sequences.";
Natl. Acad. Sci. U.S.
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oglires; Primates; Catarrhini;
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PRINTS; PR00237; GFCRHODOPSN.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Receptor; Transducer; SEQUENCE 370 AA; 41965 MW; 20DD032E716BC797 CF
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--RKSRLPREPYCVI
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US-10-318-142-2
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US-09-875-076-20
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| 45                | 44                | 43                | 42                | 41                | 40                | 39                | 38                | 37               | 36               | 35                | J<br>4           | u<br>u            | 32                | 31                | 30                | 29                | 28                |
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| 257               | 257               | 258               | 258               | 258               | 258               | 258               | 259               | 259              | 259              | 259               | 259              | 259.5             | 259.5             | 259.5             | 260               | 261.5             | 261.5             |
| 12.9              | 12.9              | 13.0              | 13.0              | 13.0              | 13.0              | 13.0              | 13.0              | 13.0             | 13.0             | 13.0              | 13.0             | 13.0              | 13.0              | 13.0              | 13.1              | 13.1              | 13.1              |
| 471               | 471               | 478               | 478               | 478               | 478               | 478               | 478               | 478              | 478              | 478               | 478              | 471               | 471               | 471               | 400               | 470               | 470               |
| 1                 | μ.                | N                 | N                 | N                 | N                 | N                 | N                 | N                | N                | N                 | N                | N                 | N                 | μ.                | N                 | N                 | N                 |
| US-08-370-542-7   | US-07-817-920-8   | US-10-176-255-31  | US-09-292-072-31  | US-09-767-013-31  | US-09-292-069A-31 | US-09-292-071-31  | US-10-176-255-33  | US-09-292-072-33 | US-09-767-013-33 | US-09-292-069A-33 | US-09-292-071-33 | US-09-145-864-4   | US-09-032-742-2   | US-07-996-772A-11 | US-09-826-509-491 | US-10-176-255-25  | US-09-292-072-25  |
| Sequence 7, Appli | Sequence 8, Appli | Sequence 31, Appl | Sequence 33, Appl | •                | •                | Sequence 33, Appl | •                | Sequence 4, Appli | Sequence 2, Appli | Sequence 11, Appl | Sequence 491, App | Sequence 25, Appl | Sequence 25, Appl |

## ALIGNMENTS

PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/120, 416
PRIOR FILING DATE: 1999-02-16
PRIOR PILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123, 946
PRIOR APPLICATION NUMBER: 60/123, 946
PRIOR APPLICATION NUMBER: 60/123, 949
PRIOR FILING DATE: 1999-03-12
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PRIOR APPLICATION NUMBER: 60/136, 439
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PRIOR APPLICATION NUMBER: 60/137, 127
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137, 127
PRIOR PILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137, 131
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PRIOR APPLICATION NUMBER: 60/156, 653
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PRIOR APPLICATION NUMBER: 60/156, 654
PRIOR APPLICATION NUMBER: 60/157, 280
PRIOR APPLICATION NUMBER: 60/157, 280
PRIOR APPLICATION NUMBER: 60/157, 281
PRIOR APPLICATION NUMBER: 60/157, 281 APPLICANT: Chen, I APPLICANT: Dang, APPLICANT: Liaw, APPLICANT: Lin, GENERAL INFORMATION: Sequence 2 Patent No. CURRENT APPLICATION NUMBER: US/09/875,076
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/417,044 APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled
FILE REFERENCE: AREN0050 20, ... 'n. 686977 Chen, Ruoping Dang, Huong T Liaw, Chen W. Application US/09875076 Receptors

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PRIOR APPLICATION NUMBER: 60/157,293
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,282
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 20
LENGTH: 373
TYPE: PRT
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US-09-622-439-6
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                                                                                                  ; TYPE: PRT
; ORGANISM: Homo
US-09-622-439-6
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SEQ ID NO 6
LENGTH: 373
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Patent No. 6555344
GENERAL INFORMATION:
APPLICANT: Yamanouchi Pharmceutical Co., Ltd.
TITLE OF INVENTION: A novel G protein coupled recepter protein
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                             Query Match
Best Local Similarity
Matches 372; Conserv
                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/622,439
CURRENT FILING DATE: 2000-08-17
ERIOR APPLICATION NUMBER: UP p1998-060245
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: UP p1999-026774
PRIOR FILING DATE: 1999-02-03
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                                   Conservative
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                                                 99.7%;
                                 Score 1986; DB 2;
Pred. No. 3.1e-170;
0; Mismatches 1;
                                                                  Length 373;
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CURRENT FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: US/09/622,439
PRIOR APPLICATION NUMBER: US/09/622,439
PRIOR APPLICATION NUMBER: JP P1998-060245
PRIOR PILING DATE: 1998-03-12
PRIOR PILING DATE: 1998-03-12
PRIOR PILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN OF SEQ ID NOS: 26
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LENGTH: 373
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Patent No. 6808899
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 3.1e-170;
0; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/09/622,439
CURRENT FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: JP P1998-060245
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: JP P1999-026774
PRIOR FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 26
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US-09-622-439-26
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Sequence 26, Application US/10318142
Patent No. 6808899
GENERAL INFORMATION:
APPLICANT: Yamanouchi Pharmceutical Co.,
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APPLICANT: Yamanouchi Pharmceutical Co.,
TITLE OF INVENTION: A novel G protein co
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Best Local Similarity
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Pred. No. 3e-169;
1; Mismatches
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ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

STREET: P.O. Box 98
CITY: Valley Forge
STATE: PA
COUNTRY: USA

ADDRESSEE:

Ratner & Prestia O. Box 980

TITLE OF INVENTION: A G-PROTEIN
TITLE OF INVENTION: (AXOR-1)
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

DERK

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7TM RECEPTOR

NABIL

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FILLE REFERENCE: Y9905
CURRENT APPLICATION NUMBER: US/10/318,142
CURRENT FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: US/09/622,439
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 1990-08-060245
PRIOR APPLICATION NUMBER: US/09/622,439
PRIOR APPLICATION NUMBER: JP 1998-060245
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: JP 1999-026774
PRIOR APPLICATION NUMBE
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US-09-251-373-2
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                                                                                                                               Sequence 2, Application US/09251373
Patent No. 6071722
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Best Local S
                                                                                              GENERAL INFORMATION:
APPLICANT: SHABON, U
APPLICANT: ELSHOURBA
APPLICANT: BERGSMA,
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Similarity 99.2%;
70; Conservative
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Best Local S
Matches 235
                                                                                Sequence 4, Application US/09622439
Patent No. 6555344
Patent INFORMATION:
APPLICANT: Yamanouchi Pharmceutical Co., Ltd.
TITLE OF INVENTION: A novel G protein coupled recepter protein
FILE REFERENCE: Y9905
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FILE REFERENCE: Y9905
CURRENT APPLICATION NUMBER: US/09/622,439
CURRENT FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: JP P1998-060245
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: JP P1999-026774
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REFERENCE/DOCKET NUMBER: GP
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/09/251 777
FILING DATE: 16-PPT CLASSIFTT.
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ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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SEQ ID NO 4
LENGTH: 370
TYPE: PRT
ORGANISM: Homo 6
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                                                                                                                                                                                         SOFTWARE: Pat
SEQ ID NO 24
LENGTH: 370
TYPE: PRT
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CURRENT FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: JP P1998-06024:
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: JP P1999-02677/
PRIOR FILING DATE: 1999-02-03
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TITLE OF INVENTION: A novel G protein coupled recepter
FILE REFERENCE: Y9905
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NUMBER OF SEQ ID NOS:
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Pred. No. 1.2e.
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SEQ ID NO 4
LENGTH: 370
TYPE: PRT
ORGANISM: Homo Bapiens
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APPLICANT: Yamanouchi Pharmceutical Co., Ltd.
TITLE OF INVENTION: A novel G protein coupled recepter protein
FILE REFERENCE: Y9905
CURRENT APPLICATION NUMBER: US/10/318,142
CURRENT FILING DATE: 2002-12-13
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PRIOR APPLICATION NUMBER: US/09/622,439
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: JP P1998-060245
PRIOR TILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: JP P1999-026774
PRIOR FILING DATE: 1999-02-03
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 SPYIVACYWRVFVKACAVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLKKCL-TTHAPCW
                                                                                      FRANDSLGFMLLLALILLATQLVYLKLIFFVHDRRKMKPVQFVAAVSQNWTFHGPGASGQ
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US-10-318-142-24
                                           Sequence 26, Application US/09875076 Patent No. 6869776 GENERAL INFORMATION:
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APPLICANT: Chen, Ruoping
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
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CURRENT APPLICATION NUMBER: US/10/318,142;
CURRENT FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: US/09/622,439
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: UP P1998-060245
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: UP P1999-026774
PRIOR FILING DATE: 1999-02-03
PRIOR FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 24
LENGTH: 370
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Best Local Similarity
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358 --RKSRLPREPYCVI 370
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Pred. No. 1.2e-107;
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CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/417,044
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APPLICATION NUMBER: 60/156,653
PTITING DATE: 1999-09-29
PTITING DATE: 1999-09-29
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PARTICATION NUMBER: 09/417,044
FILING DATE: 1999-10-12
APPLICATION NUMBER: 60/120,416
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APPLICATION NUMBER: 60/157,294
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                                                    RYMAIAHHRFYAKRMTLWTCAAVICMAWTLSVAMAFPPVFDVGTYKFIREEDQCIFEHRY 180
                                                                                    MANYSHAADNILQNI.SP--LTAFLKLTSLGFIIGVSVVGNLLISILLVKDKTLHRAPYYF
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US-09-622-439-2
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US-10-318-142-2
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LENGTH: 375
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     Sequence 2, Application US/10318142
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ORGANISM: Homo
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FILE REFERENCE: Y9905
FILE REFERENCE: Y9905
CURRENT APPLICATION NUMBER: US/09/622,439
CURRENT FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: JP P1998-060245
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: JP P1999-026774
PRIOR FILING DATE: 1999-02-03
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                                LLLWSPYIVACYWRVEVKACAVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLKKCLTTHA
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ON: A novel G protein coupled recepter protein
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Pred. No. 1.5e-84;
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APPLICANT: LYMANICAL PHARMCEUTICAL CO., LE.
APPLICANT: LYMANICON: A novel G protein couple
FILE REFERENCE: Y9905
CURRENT APPLICATION NUMBER: US/10/318,142
CURRENT FILING DATE: 2002-12-3
PRIOR APPLICATION NUMBER: US/09/622,439
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: JP P1999-026774
PRIOR FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
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FILE REFERENCE: ARENOOSO
CURRENT APPLICATION NUMBER: US/09/875,076
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR PRIOR APPLICATION NUMBER: 60/121,851
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
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US-10-318-142-2
                                                                                                                                                                                                                                           Patent No. 6869776
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             Sequence 16,
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                                                                                                                                                 APPLICANT: Chen, Ruoping
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
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Pred. No. 1.5e-84;
2; Mismatches 92;
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Best Local S
Matches 196
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LENGTH: 375
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SOFTWARE: PatentIn Ver.
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PRIOR FILING DATE: 1999-10-01
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ORGANISM: Homo sapiens
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APPLICATION NUMBER: 60/
FILING DATE: 1999-10-01
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APPLICATION NUMBER: 60/137,131
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APPLICATION NUMBER: 60/136,439
FILING DATE: 1999-05-28
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FILING DATE: 1999-03-12
APPLICATION NUMBER: 60/136,436
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APPLICATION NUMBER: 60/157,280
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APPLICATION NUMBER: 60/156,633
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APPLICATION NUMBER: 60/156,653
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                                              LLLWSPYIVACYWRVFVKACAVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLKKCLTTHA
PC 357
                              ATGOAAANWTAGFGRGPTPPALVGIRPAGPGRGARRLLVLEEFKTEKRLCKMFYAVTLLF
                                                                                                                   ATGQAAANWIAGFGRGPMPPTLLGIRQNGHA-ASRRLLGMDEVKGEKQLGRMFYAITLLF
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54.1%; Pred. No. 1.5e-84;
tive 62; Mismatches 92
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Sequence 22, Application US/09622439

Sequence 22, Application US/09622439

Patent No. 6555344

GENERAL INFORMATION:

APPLICANT: Yamanouchi Pharmceutical Co., Ltd.

TITLE OF INVENTION: A novel G protein coupled recepter protein

FILE REFERENCE: Y9905

CURRENT PELICATION NUMBER: US/09/622,439

CURRENT FILING DATE: 2000-08-17

PRIOR APPLICATION NUMBER: UP P1998-060245

PRIOR APPLICATION NUMBER: UP P1998-060245

PRIOR APPLICATION NUMBER: UP P1998-026774

PRIOR FILING DATE: 1998-03-12

PRIOR FILING DATE: 1999-026774

PRIOR FILING DATE: 1999-02-03

NUMBER OF SEQ ID NOS: 26

SOFTMARE: Patentin Ver. 2.0

SEQ ID NO 22

LENGTH: 377

TYPE: PRT

ORGANISM: Rattus Sp.

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Search completed: March
Job time : 47 secs
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Adh68272 Adg12840 Ado28774 Adx44593 Ady8382 Ady93947 Aay90537 Aay90537 Aay54323 Aay85145 Aab02817 Aay71303 Aay7130 Aay

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12-NOV-1998;
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27-NOV-1998;
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01-OCT-1999;
01-OCT-1999;
01-OCT-1999;
12-OCT-1999;
12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes transmembrane receptors, preferably hums grotein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present inventior relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 373
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                                                          AAY71300
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The present amino acid sequence is the hARE-2, an endogenous human orphan CC g protein-coupled receptor (GPCR), expressed in the left and right CC cerebellum. The hARE-2 cDNA was identified using ESTs (expressed sequence CC tag) A1090920 and 68530 as a probe. The orphan GPCR of the invention, CC like all GPCRs has seven transmembrane alpha helices with an CC entracellular N-terminus and an intracellular C-terminus. However, no CC entogenous ligands has yet been identified for the proteins of the CC invention. The orphan GPCRs may be used in the identification of their CC entogenous ligands, and to screen potential GPCR agonists and antagonists CC entogenous ligands, and to screen potential GPCR agonists and antagonists CC entogenous ligands, and to screen potential GPCR agonists and antagonists CC eruse as pharmaceutical agents. The proteins may also be used in the CC study of GPCR-mediated signalling cascades, and to elucidate their CC precise role in normal and diseased human conditions. Nucleic acid cencoding human orphan GPCRs may be used for tissue localisation in CC expression analysis to provide information about their function in CC healthy and pathological states
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Sequence
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DB; AAD01127.
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373;

h 100.0%; Score 1992; DB 3; Similarity 100.0%; Pred. No. 6.1e-218; 73; Conservative 0; Mismatches 0;

Indels Length

Gaps

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Novel endogenous, orphan, human G protein-coupled receptors useful identification of modulators of the receptor and as research tools understanding the role of the receptor in human body.
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N-PSDB; ACA93265.
                                                                                                                                            Claim
                                                                                                                                           38; Page 27-28; 54pp; English.
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The invention relates to a human G protein-coupled receptor (GPCR) CC appearing as ABU92259-ABU92277 (encoded by cDNAs ACA93256-ACA93274) named CC hARE-3, hARE-4, hARE-5, hRU93, hRUP6, hRUP7, hGPCRZ7, hARE-1, hARE CC -2, hPR1, hC2A, hCHN3, hCHN4, hCHN6, hCHN9, hCHN9 hCHN10 and hRUF4. CC Also included are a plasmid comprising a vector and one of the cDNAs above and a host cell comprising the plasmid. The GPCRs are useful for the direct identification of candidate compounds as inverse agonists, agonists or partial agonists. In vitro and in vivo systems incorporating CC GPCRs is useful for elucidating and understanding the roles these creceptors play in the human condition, both normal and diseased, as well as understanding the role of constitutive activation as it applies to understanding the signalling cascade. The cDNAs are useful for making a cropbe for dot-blot analysis against tissue mRNA and/or RT-PCR corporative represents a GPCR of the invention

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Query Match
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Matches 373; Conserv
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 100.0%; Score 1992; DB 6; 100.0%; Pred. No. 6.1e-218; tive 0; Mismatches 0;
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                                                                PYIVACYMRVFVKACAVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLKKCL
                                                                                                  PYIVACYWRVFVKACAVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLKKCLTTHAPCWGT
                                                                                                                                                      AAANWIAGFGRGPMPPTLLGIRQNGHAASRRLLGMDEVKGEKQLGRMFYAITLLFLLLWS
                                                                                                                                                                                                                        FKANDTLGFMLMLAVLMAATHAVYGKLLLFEYRHRKMKPVQMVPAISQNWTFHGPGATGQ
                                                                                                                                                                                                                                                                            RYMAIAHHRFYAKRMTLWTCAAVICMAWTLSVAMAFPPVFDVGTYKFIREEDQCIFEHRY
                                                                                                                                                                                                                                                                                                                                              LLDLCLADGIRSAVCFPFVLASVRHGSSWTFSALSCKIVAFMAVLFCFHAAFMLFCISVT
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                                                                                                                                  AAANWIAGFGRGPMPPTLLGIRQNGHAASRRLLGMDEVKGEKQLGRMFYAITLLFLLLWS
                                                                                                                                                                                                        FKANDTLGFMLMLAVLMAATHAVYGKLLLFEYRHRKMKPVQMVPAISQNWTFHGPGATGQ
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RESULT 4
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ID ADG9
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AC ADG9
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DT 11-M
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DE Huma
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XW Huma
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OS Homco ADG98766

ADG98766 standard;

protein;

373 B

11-MAR-2004 (first entry

Human orphan GPCR protein, ARE-2.

Human; G protein-coupled receptor; GPCR; research tool; receptor.

Homo sapiens

US2003148450-A1

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Matches 373
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112-MAR-1999
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28-MAY-1999
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28-SEP-1999
29-SEP-1999
29-SEP-1999
                                                                                                                                                                                                                                                                                           The present invention provides novel human G protein-coupled receptor (GPCR) proteins and their encoding nucleic acids. The invention is useful for making a probe for dot-blot analysis and for RT-PCR identification of the expression of the receptor in tissue samples. The invention is also useful for identifying candidate compounds as inverse agonists, agonists or partial agonists and as research tools in determining the location of the receptors within the body. The present sequence is human orphan G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                             New cDNA encoding a human G protein coupled receptor, useful for making probe for dot-blot analysis against tissue-mRNA, and/or for RT-PCR identification of the expression of the receptor in tissue samples.
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(DANG/)
(LIAW/)
(LINI/)
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16-FEB-1999;
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                                                                                                                                                                                                                                                                         Sequence 373 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 38; SEQ ID NO 20; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
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)B; ADG98765.
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                                                                                                                                             LLDLCLADGIRSAVCFPFVLASVRHGSSWTFSALSCKIVAFMAVLFCFHAAFMLFCISVT
                                                                                                                                                                               MANTTGEPEEVSGALSPPSASAYVKLVLLGLIMCVSLAGNAILSLLVLKERALHKAPYYF
AAANWIAGFGRGPMPPTLLGIRQNGHAASRRLLGMDEVKGEKQLGRMFYAITLLFLLLWS
                                                                                                                                 LLDLCLADGIRSAVCFPFVLASVRHGSSWTFSALSCKIVAFMAVLFCFHAAFMLFCISVT
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                                                   FKANDTLGFMLMLAVLMAATHAVYGKLLLFEYRHRKMKPVQMVPAISQNWTFHGPGATGQ
                                                                                    RYMAIAHHRFYAKRMTLWTCAAVICMAWTLSVAMAFPPVFDVGTYKFIREEDOCIFEHRY
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99US-0121852P
99US-0123946P
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99US-0136436P
99US-0136437P
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99US-0136567P
99US-0137127P
99US-0137127P
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99US-0156333P
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Pred. No. 6.1e-218;
                                                                                                                                                                                                                             Mismatches
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Claim

38;

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RESULT 5
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                                                                                           (CHEN/)
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                                                                                                                                                                                                                                                                                                                                                                         Human; G protein-coupled receptor; GPCR; dot-blot analysis;
pharmaceutical agent; receptor.
                                                                                                                                                                                                                                                                                                                                                                                               Human endogenous orphan G-protein
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                          disease or disorder candidate compounds
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                                                         N-PSDB;
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                                 G protein-coupled receptor and its coding r disorder identification and/or selection.
                                                                                                                               99US-0120416P.
99US-0123946P.
99US-0123946P.
99US-0136436P.
99US-0136437P.
99US-0136437P.
99US-0137127P.
99US-0137127P.
99US-0137123P.
99US-0156533P.
99US-015653P.
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and
                            useful for screening of in research
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Matches 373;
13-OCT-1998;
12-NOV-1998;
20-NOV-1998;
27-NOV-1998;
27-NOV-1999;
16-FEB-1999;
12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to human endogenous orphan G protein-coupled receptor (GPCR) proteins and polynucleotides encoding such proteins. The cDNA sequence of the human G protein-coupled receptor (GPCR) is useful in making a probe for dot-blot analysis against tissue-mRNA and/or for RT-PCR identification of the expression of the receptor in tissue. Samples. GPCR sequences of the invention may be used in disease/disorder identification and/or selection, in screening of candidate compounds for use as pharmaceutical agents and in research settings. The present sequence is human endogenous orphan GPCR protein.
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                                                                                                                                                                                                                                       Human endogenous orphan GPCR hARE-2.
                                                                                                                                                                                                                                                                   11-MAR-2004
                                                                                                    16-APR-2003;
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                                                                                                                                                                                                     transmembrane
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                                                                                                                                                                                                                 receptor; endogenous
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98US-00170496.
98US-0108029P.
98US-01109213P.
98US-0110060P.
99US-0120416P.
99US-0121852P.
99US-0123944P.
                                                                                                                                                                                                      domain
                                                                                                                                                                                                                                                                                                                    protein;
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No. 6.1e-218;
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The invention relates to a cDNA encoding a non-endogenous, constitutively cativated version of a human G protein-coupled receptor comprising hARE-3 (P313K), hARE-4 (P233K), hARE-5 (A240K), hGPCR14 (L257K), hGPCR27 (C283K), hARE-1 (E232K), hARE-2 (G285K), hPPR1 (L239K), hGPCR14 (L257K), hRUP3 (L224K), hRUP5 (A236K), hAUP6 (W267K), hRUP7 (A302K), hCHN4 (V236K), hRUP3 (L224K), hCHN4 (V236K), hRUP3 (L224K), hCHN4 (W236K), hRUP3 (M252K), hRUP
        Query Match
Best Local S
Matches 373
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12-MAR-1999
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29-JUN-1999
27-JUN-1999
28-P-1999
29-SEP-1999
29-SEP-1999
29-SEP-1999
29-SEP-1999
21-OCT-1999
01-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor, useful for identifying receptor, inverse or partial agonists having potential applicability as therapeutic
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                                                                                  Sequence
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(LOWI/)
(CHAL/)
(BEHA/)
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DB; ADG86382.
          373;
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LIAW C W.
LOWITZ K.
CHALMERS D T.
BEHAN D P.
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nilarity 100.
Conservative
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                                                                                    AA;
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99US-0123948P.
99US-0123949P.
99US-0123951P.
99US-0136437P.
99US-0136437P.
99US-0137127P.
99US-0137127P.
99US-0137131P.
99US-01571144P.
99US-0156534P.
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13-OCT-1998

12-NOV-1998

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26-FEB-1999

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29-UN-1999

29-SEP-1999

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20-SEP
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G protein-coupled receptor; GPCR; GPCR modulator; inflammation;
pharmaceutical composition; inflammatory disorder; human; hARE-2.
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99US-0137137P
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AAANWIAGFGRGPMPPTLLGIRQNGHAASRRLLGMDEVKGEKQLGRMFYAITLLFLLLWS

**FKANDTLGFMLMLAVLMAATHAVYGKLLLFEYRHRKMKPVQMVPAISQNWTFHGPGATGQ** FKANDTLGFMLMLAVLMAATHAVYGKLLLFEYRHRKMKFVQMVFAISQNWTFHGFGATGQ RYMAIAHHRFYAKRMTLWTCAAVICMAWTLSVAMAFPPVFDVGTYKFIREEDQCIFEHRY RYMAIAHHRFYAKRMTLWTCAAVICMAWTLSVAMAFPPVFDVGTYKFIREEDQCIFEHRY LLDLCLADGIRSAVCFPFVLASVRHGSSWTFSALSCKIVAFMAVLFCFHAAFMLFCISVT

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LLDLCLADGIRSAVCFPFVLASVRHGSSWTFSALSCKIVAFMÄVLFCFHÄAFMLFCISVT

62 61 Н

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PYIVACYWRVFVKACAVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLKKCI

PYIVACYWRVFVKACAVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLKKCLTTHAPCWGT

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The invention describes a method of identifying one or more candidate compounds as a modulator of a G protein-coupled receptor that comprises a CC compounds as a modulator of a G protein-coupled receptor that comprises a CC fully defined sequence of 337 amino acids (SEQ ID NO: 82), comprising CC contacting the one or more compounds with a host cell or with a membrane CC of a host cell that expresses the receptor, and measuring the ability of the compound or compounds to inhibit or stimulate functionality of the creceptor. Also described are: a method for identifying one or more candidate compounds as a modulator of inflammation; a method for coupled receptor; a compound identified by any of the methods cited compoused receptor; a compound identified by any of the methods cited cabve; a pharmaceutical composition; a method of modulating the activity of a G protein-coupled receptor having the amino acid sequence of SEQ ID CC NO.82; a method of modulating inflammation in a mammal in need of the inhibiting; a method of preventing or treating an inflammatory classified by any of the sequence of the inhibiting; a method of preventing or treating an inflammatory classified of the preventing or treating; and a method confident in a mammal in need of the inhibiting an inflammatory disorder. The methods and compositions of the greent invention are useful for the treatment of diseases or conditions of inflammation. This is the amino acid sequence of human G protein coupled confident of the prevention are useful for the treatment of diseases or conditions associated with aberrant expression or activity of the GPCR e.g.
  Query Match
Best Local S
Matches 373
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01-OCT-1999;
12-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying one or more candidate compounds as a modulator of a G protein -coupled receptor (GPCR), useful for treating disorders or conditions associated with expression or activity of the GPCR.
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(LIAW/)
(LOWI/)
(CHAL/)
                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 22; 106pp; English.
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LIAW C W.
LOWITZ K.
CHALMERS
h 100.0%; Score 1992; DB 8; Similarity 100.0%; Pred. No. 6.1e-218; 73; Conservative 0; Mismatches 0;
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29-SEP-1999;
01-OCT-1999;
01-OCT-1999;
01-OCT-1999;
The invention relates to identifying one or more candidate compounds as modulators of a G protein-coupled receptor comprising an endogenous human ARE-2 polypeptide (appearing as AD075080) comprises measuring the ability of the compound or compounds to inhibit or stimulate functionality of the receptor. The endogenous human ARE-2 polypeptide is encoded by a nucleotide sequence, the nucleotide properties is encoded by a nucleotide sequence, the nucleotide of human DNA library using specific probe EST (expressed sequence tag) clone 68530, where the amino
                                                                                                                                                                                                                                                            Identifying one or more candidate compounds as modulators of a G protein-coupled receptor, useful as pharmaceutical agents, comprises measuring the ability of the compound or compounds to inhibit or stimulate functionality of the receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                G protein-coupled receptor protein; inflammatory disorder; immunologica
                                                                                                                                      12-MAR-1998;
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N-PSDB; AAZ10562.
                                                                                                                                                                                                   Monalisa; human; G-protein coupled receptor; infection; 1 HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; hypotension; Parkinson's disease; acute heart failure; hypertension; osteoporosis; urinary retention; angina pectoris; myocardial infarction; stroke; ulcer; allergy; benign prostatic hypertrophy; migratine; psychotic disorder; neurological disorder; anxiety; achizophrenia; manic depression; delirium; dementia; severe mental retardation; dyskinesia; therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Human MonaLisa protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY97747
                                                            WO200132833-A2
                                                                                                                                                                           Huntington's disorder; Gilles dela Tourette's syndrome
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Pred. No. 3e-217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is the human Monalisa protein of the invention. The Monalisa protein is a member of the G-protein coupled receptor family. The Monalisa polypeptide and polynuclectide are useful for treating infections e.g. bacterial, fungal or viral infections particularly those caused by HIV-1 or HIV-2. The Monalisa sequences are also useful for treating pain, cancers, diabetes, obesity, anorexia, bulimia, asthma, carking pain, cancers, diabetes, obesity, anorexia, bulimia, asthma, carking pain, cancers, diabetes, obesity, anorexia, bulimia, asthma, carking, retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, schizophrenia, manic depression, delirium, dementia, and severe mental retardation), dyskinesias, Huntington's disorder, and Gilles dela creative's syndrome. The Monalisa polypeptide and polypuncleotide are also useful in diagnostic assays, as well as in identifying compounds (e.g. agonists or antagonists) that are potentially useful in therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New MonaLisa G-protein coupled receptor polypeptides and polynucleotides, useful for treating certain diseases (e.g. infections, pain or cancers), in diagnostic assays, or for identifying compounds for therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 373
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                         GGAPAPREPYCVM
                                                                                           PYIVACYWRVEVKACAVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLKKCLTTHAPCWGT
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99.7%;
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Pred. No. 3e-217;
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ABP81720 ID ABP8

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standard;

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ABP81720;

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The present invention describes antigenic peptides (I) comprising: (a) cany one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino CC acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample: CC and (2) an isolated antibody having high specificity and high affinity or CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an CC antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for detecting the CC gresence or absence of corresponding GPCRs. The antigenic peptides for CC GPCRs and antibodies are useful for diagnosing and designing drugs for CC treating immune-related diseases, growth-related diseases, cell CC diseases, or autoimmune diseases, growth-related diseases, cell cost costion, altergise, Crohn's disease, Alzheimer's disease, datheroscierosis, bacterial, fungal, protozoan or viral infections, CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, altergise, Crohn's disease, diabetes, graft versus host CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, cancer, cardiomyopathy, chronic and acute of the present of the present involved. The antibodies may be CC used in immunoassays and immunodiagnosis. ABZ45231 to ABZ4269 encode CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
Query Match
Best Local Similarity
                                                            Sequence 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy
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Score
Pred.
1986; DB 6;
No. 3e-217;
                   Length 373;
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analgesic; anorectic; antiparkinsonian; nootropic; neuroprotective;
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CC which alters G protein coupled receptor (GPCR) internalisation. The CC method comprises providing a cell comprising a GPCR, an arrestin, and a CC modified G protein coupled receptor kinase (GRK), exposing the cell to CC arrestin, or modified GRK, and monitoring a difference between the CC distribution of the GPCR, arrestin, or modified GRK in the GPCR, arrestin, or modified GRK in the cell in the CC distribution of the GPCR, arrestin, or modified GRK in the cell in the CC presence and absence of the compound. The GPCR in the method described CC above is at least partially internalised in an agonist-independent manner CC distribution of the GRK. (I) has cardiant, cardiovascular, CC antiasthmatic, respiratory, antiinflammatory, antiallergic, anorectic, antiparkinsonian, nootropic, antidepressant, CC analgesic, anorectic, antiparkinsonian, nootropic, neuroprotective, CC analgesic, anorectic, antiparkinsonian, nootropic, neuroprotective, CC immunosuppressive and cytostatic activities, and can be used as a GC protein antagonist. The methods and compositions of the present invention CC desensitisation, such as angina pectoris, essential hypertension, CC myocardial infarction, arrhythmias, congestive heart failure, CC atherosclerosis, renal failure, diabetes, asthma, chronic bronchitis, constric ulcers, pain, obesity, depression, obsessive-compulsive disease, failure, disease, multiple sclerosis and cancer. The present sequence is used in the exemplification of the present
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Best Local :
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GGAPAPREPYCVM 37:
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muscular disorder; blood disorder; immune disorder; bone disorder; joint disorder; metabolic disorder; mutritive disorder; cancer; kidney disorder; liver disorder; liver disorder; breast disorder; sylver disorder; liver disorder; breast disorder; ovary disorder; uterus disorder; prostate disorder; testis disorder; skin disorder; stomach disorder; pancreas disorder; spleen disorder; thymus disorder; thyroid disorder; antiparkinsonian; antimanic; cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic; cytostatic; antivole; vespiratory; antidiarrhoeic; antidiabetic; virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic; dermatological; antiulcer; antithyroid; antiallergic; anorectic; immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G protein-coupled receptor; GPCR; drug screening; diagnosis; transgenic mouse; neurological disorder; adrenal gland disorder; colon disorder; intestinal disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human novel GPCR SREB3, SEQ
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Gaitanaris GA, Bergmann Madisen L, Mcilwain KL, 09-SEP-2002; 2002US-0409303P. 09-APR-2003; 2003US-0461329P. 09-SEP-2003; 2003WO-US028226. 13-MAY-2004 (PRIM-) PRIMAL INC JE, Gragerov Pavlova MN, A, Hohmann Vassilatis I á ŗ

Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina WPI; 2004-390329/36. N-PSDB; ADO29792.

Claim 1; SEQ ID NO 243; 542pp; English. pectoris,

Parkinson's disease.

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CRORRED and nucleic acids encoding them. The invention also relates to compensation relates to human and mouse G protein-coupled receptors CC (GPCRE) and nucleic acids encoding them. The invention also relates to compensate the control of treatment of GPCR proteins and nucleic acids control of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic compounds useful in the treatment of GPCR-related diseases; a transgenic computation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has comparison in a different GPCR gene of the invention; and kits comprising comprising the comprision of a mutation in a different GPCR gene of the invention; and kits comprising comprising the comprising comprising a gPCR gene of the invention; and kits comprising comprising a gPCR mucleic acid. The GPCR polymclectides of the invention. The comprising a gPCR mucleic acid. The GPCR polypeptides and vectors comprising a gPCR mucleic acid. The GPCR polypeptides and vectors comprising a gPCR mucleic acid. The GPCR polypeptides and vectors comprising a gPCR mucleic acid. The GPCR polypeptides and vectors comprising a gPCR mucleic acid. The GPCR mucleic acids and proteins may comprise the disposis, treatment or prevention of a wide variety of comprising a gPCR mucleic acid. The GPCR mucleic acids and proteins may compression, diabetic neuropathy, parkinson's disease or schizophrenia); conditions disease, disarrhoes, food poisoning or irritable bowel composition or intestine compression or interestine control of the colon or intestine control of the colon or intes anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g. obesity, enzyme deficiency-related diseases or vitamin deficiency-related deficiency-related disorders (e.g

RESULT 13 ADO29142 ID ADO29

ADO29142 standard; protein; 373 AA

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KW Antis
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Best Local Si
Matches 372;
                                                                                                                                                                                                                                                                                                          Respiratory-Gen.; Neuroprotective; Gynecological; Nootropic; Antialermit; Hypotensive; Antialcer; Cardiant; Antiallergic; Neuroleptic; Muscular-Gen.; Antidepressant; Gynotein coupled receptor inhibitor; Gynotein coupled receptor activator; SREB3; diagnosis; Gynotein coupled receptor activator; SREB3; diagnosis; Cardiovascular disease; Endocrine disease; Genitourinary disease; Andrology; Gynecology and obstetrics; Hematological disease; Respiratory Metabolic disorder; Neoplasm; Neurological disease; Respiratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cardiovascular-Gen.; Cytostatic; Endocrine-Gen.; Antianemic; Respiratory-Gen.; Neuroprotective; Gynecological; Nootropic; Antiasthmatic; Hypotensive; Antiulcer; Cardiant; Antiallergic;
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Cwith G protein coupled receptor SREB3 polypeptide. The method is useful

CC for screening, diagnosing or treating cardiovascular disease, cancer,

CC endocrinological disease, metabolic disease, hematological disease,

CC respiratory disease, neurological disease, urological disease or

CC reproduction disease in mammals. Also useful for treating hypertension,

CC ulcer, myocardial infarction, asthma, allergise, depression,

CC schizophrenia, dyskinesia, delirium and dementia. The method provides the

CC screening of an agent for the treatment of a wide variety of disease,

CC including cardiovascular disease, cancer, endocrinological disease,

CC metabolic disease, hematological disease, respiratory disease,

CC meurological disease, urological disease or reproduction disease, by

CC detecting the binding and/or activity with a G protein coupled receptor,

CC SREB3 that is highly expressed in various brain tissues. The present
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Matches 372
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| 000US-0226681 000US-0226681 000US-0226881 000US-0227182 000US-022934 000US-0229343 000US-0229343 000US-0229343 000US-0229343 000US-0229343 000US-0231242 000US-0231243  | expressed polypeptide SEQ ID NO 77.  nontropic; neuroprotective; cytostatic; dermatological; virucide; nontropic; neuroprotective; anti-HIV; antibacterial; vulnerary; riskinsonian; antisicking; antianaemic; antiarthritic; cancer; pleumatic; hepatotropic; cerebroprotective; antiarthritic; cancer; pleumatic; natidiaberic; antiulcer; antiarthritic; cancer; pleumatic; antidiaberic; antiulcer; anticonvulsant; antifungal; latinitic; cardiant; immune disorder; cardiovascular disorder; cardiovascula   | standard; protein; 378 AA.   |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel genes (AAI99548-AAI99604) and proteins (C (AAM99936, AAM99984) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are c isolated from a range of human tissues disclosed in the specification. C The nucleic acids, proteins, antibodies and (ant)agonists are useful in the disgnosis, treatment and prevention of: (a) cancer, e.g. breast and covarian cancer and other cancers of the adrenal gland, bone, bone marrow, c breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune C disorders e.g. Addison's disease, allergies, autoimmune haemolytic c anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, c multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) c ardiovascular disorders such as myocardial ischaemias; (d) wound healing (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) c infectious diseases such as viral, bacterial, fungal and parasitic c infectious diseases such as viral, bacterial, fungal and parasitic c infectious diseases such as viral, bacterial, fungal and parasitic c infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly c from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                   Query Match Best Local Similarity Matches 372; Conserv
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08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated digestive system associated polypeptide for treating, preventing and/ or prognosing disorders related to the digestive system including digestive system cancers and also for testing and detection e.g. diagnosis.
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N-PSDB; AAI99565.
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                    AAANWIAGFGRGPMPPTLLGIRQNGHAASRRLLGMDEVKGEKQLGRMFYAITLLFLLLWS
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2000US-0251919P.
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Pred. No. 3e-217;
0; Mismatches 1;
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Search completed: March 7, 2006, 12:50:16
Job time: 188 secs

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Pred. No: is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| 29                 | 28     | 27     | 26                | 25                 | 24                 | 23                 | 22                 | 21     | 20                | 19                 | 18                 | 17                 | 16                 | 15                 | 14                 | 13                | 12     | 11     | 10                 | 9                  | 8                  | 7                  | 6      | Ŋ      | 4.     | ω      | 2      | _    | Result      |
|--------------------|--------|--------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------|--------|------|-------------|
| 231.5              | 232    | 233    | 234               | 235                | 236                | 236                | 236                | 237    | 237               | 238.5              | 241.5              | 243                | 243.5              | 244                | 247                | 247.5             | t n    | 256)   | 256.5              | 257                | 259.5              | 55                 | 259.5  | 260    | 264    | 1031   | 1288.5 | 8    | Score       |
| 11.6               | 11.6   | 11.7   | ۲                 | 11.8               | ۲                  | 11.8               | 11.8               | 11.9   | 11.9              | •                  | 12.1               | •                  | ٠                  | 12.2               | 12.4               | 12.4              | •      |        | 12.9               | •                  | 13.0               | 13.0               | 13.0   | 13.1   | 13.3   | 51.8   | 64.7   | 99.7 | Query       |
| 458                | 460    | 377    | 446               | 445                | 483                | 481                | 481                | 477    | 446               | 450                | 450                | 448                | 447                | 448                | 452                | 387               | 453    | 400    | 471                | 471                | 471                | 471                | 449    | 400    | 387    | 375    | 370    | 373  | Length      |
| N                  | N      | N      | N                 | N                  | ผ                  | N                  | N                  | N      | _                 | N                  | N                  | N                  | N                  | N                  | N                  | _                 | N      | N      | N                  | N                  | N                  | N                  | N      | N      | N      | N      | N      | N    | BB          |
| JS0616             | A32605 | S68423 | I48322            | A48881             | A25896             | S43687             | S49442             | S71323 | DYRTD3            | A34169             | 840392             | A47519             | A47430             | S36402             | JC2459             | DYHUD4            | S32817 | G00013 | A34863             | A43956             | S40689             | S11280             | S02011 | G01977 | I49246 | JC7287 | T47131 | 72   | ID          |
| serotonin receptor |        |        | dopamine receptor | serotonin receptor | beta-adrenergic re | serotonin receptor | serotonin receptor |        | dopamine receptor | alpha-2A-adrenergi | alpha-2-adrenergic | serotonin receptor | gastrin/cholecysto | serotonin receptor | gastrin/cholecysto | dopamine receptor |        | 3      | serotonin receptor | serotonin receptor | 5-hydroxytryptamin | serotonin receptor | Œ      |        | 3      |        | ä      |      | Description |

|                    |                    | 43 224.5           |                    |                    | 40 225.5          |                    |                    | 37 226.5           |                   |                   |                    |                    |                    | 31 231            |                   |
|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|
| 11.2               | 11.2               | 11.3               | 11.3               | 11.3               | 11.3              | 11.3               | 11.3               | 11.4               | 11.4              | 11.4              | 11.4               | 11.5               | 11.5               | 11.6              | 11.6              |
| 504                |                    |                    |                    |                    |                   |                    |                    | 450                |                   |                   |                    |                    |                    | 466               | 464               |
| 2                  |                    | 2                  |                    | _                  | _                 |                    |                    | 22                 |                   |                   |                    |                    |                    | 2                 | 8                 |
| A41783             | JC6178             | A43951             | A47321             | T37240             | QRHUB1            | 149481             | JQ1614             | A38316             | JC5599            | 151898            | 138209             | JN0692             | A31237             | S36794            | S12591            |
| tachykinin recepto | serotonin receptor | serotonin receptor | serotonin receptor | serotonin receptor | beta-1-adrenergic | alpha-2 adrenergic | gastrin receptor - | alpha-2-adrenergic | cholecystokinin-A | cholecystokinin A | serotonin receptor | cholecystokinin ty | alpha-2C-adrenergi | beta-1-adrenergic | beta-1-adrenergic |

## ALIGNMENTS

| дь                    | 8                     | ДĎ   | S  | Дb   | Q  | Ф  | Ş  | рь   | 8  | Db  | SS.   | DЬ  | ρ   | Quer<br>Best<br>Matcl  | A;Gei<br>A;Maj<br>C;Suj<br>C;Key  | A)Cr | A; Mo.   | A; Ac  | A;Title:  | R;Mai                                | C;Dal  | G-prot | RESULT |
|-----------------------|-----------------------|--|--|--|--|--|--|--|--|---|---|---|---|--|---|------|--|--|---|--------------------------------------|--|--------|--------|
| 361 GGAPAPREPYCVM 373 | 361 GGAPAPREPYCVM 373 | 301 PYIVACYMRVFVKACAVPHRYLATAVMMSFAQAAVNPIVCFLLNKDLKKCLRTHAPCWGT 360 | 301 PYIVACYMRVFVKACAVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLKKCLTTHAPCWGT 360 | 241 AAANWIAGFGRGPMPPTLLGIRQNGHAASRRLLGMDEVKGEKQLGRMFYAITLLFLLLMS 300 | 241 AAANWIAGFGRGPMPPTLLGIRQNGHAASRRLLGMDEVKGEKQLGRMFYAITLLFLLLWS 300 | 181 FKANDTLGEMLMLAVLMAATHAVYGKLLLFEYRHRKMKFVQMVPAISQNWTFHGPGATGQ 240 | 181 FKANDTLGEMLMLAVLMAATHAVYGKLLLFEYRHRKMKPVQMVPAISQNWTFHGPGATGQ 240 | 121 RYMAIAHHREYAKRMTLMTCAAVICMAWTLSVAMAFPPVFDVGTYKFIREEDQCIFEHRY 180 | 121 RYMAIAHHRFYAKRMTLWTCAAVICMAWTLSVAMAFPPVFDVGTYKFIREEDQCIFEHRY 180 | 61 LIDLCLADGIRSAVCFPFVLASVRHGSSWTFSALSCKIVAFWAVLFCFHAAFMLFCISVT 120 | 61 LLDLCLADGIRSAVCFPFVLASVRHGSSWTFSALSCKIVAFMAVLFCFHAAFMLFCISVT 120 | 1 MANTTGEPEEVSGALSPPSASAYVKLVILGLIMCVSLAGNAILSLLVLKERALHKAPYYF 60 | 1 MANTTGEPEEVSGALSPPSASAYVKLVLLGLIMCVSLAGNAILSLLVLKERALHKAPYYF 60 | Query Match 99.7%; Score 1986; DB 2; Length 373; Best Local Similarity 99.7%; Pred. No. 8.1e-174; Matches 372; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | A;Gene: sreb3<br>A;Map position: Xp11<br>C;Superfamily: endothelin receptor B<br>C;Keywords: brain; G protein-coupled receptor; glycolysis; reproduction; transmembrane ] |      | A;Molecule type: mRNA<br>A;Residues: 1-373 <mat></mat> | A;Reference induser: JC/28/<br>A;Accession: JC7289 | A;Title: An evolutionarily conserved G-protein coupled receptor family, SREB, expressed | oto, M.; Saito, T.; Takasaki, J.; Ka | C;bpecies: nomo saplens (man)<br>C;Date: 18-Aug-2000 | ein    | LT 1   |

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A;Cross-references: UNIPROT:P60893; UNIPARC:UPI0000004048; EMBL:AL161959; NID:g7328012; A;Experimental source: adult amygdala; clone DKFZp761L08121
R;Matsumoto, M.; Saito, T.; Takasaki, J.; Kamohara, M.; Sugimoto, T.; Kobayashi, M.; Tac Blochem. Biophys. Res. Commun. 272, 576-582, 2000
A;Title: An evolutionarily conserved G-protein coupled receptor family, SREB, expressed A;Reference number: JC7287
A;Accession: JC7288
RESULT 3
JC7287
G_Protein coupled receptor, SREB1 - human
G_Protein coupled receptor, SREB1 - human
C;Species: Homo sapiens (man)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: JC7287
R;Matsumoto, M: Saito, T:; Takasaki, J.; Kamohara, M.; Sugimoto, T.; Kobayashi, Biochem. Biochys. Res. Commun. 272, 576-582, 2000
A;Title: An evolutionarily conserved G-protein coupled receptor family, SREB, exp. A;Reference number: JC7287
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A;Note: DKFZp761L08121.1
C;Keywords: brain; G pro
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A;Residues: 1-370 <MAT>
A;Cross-references: UNIPARC:UPI0000004048; DDBJ:AB040799
C;Genetics:
A;Gene: sreb2
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A;Accession: T47131
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Best Local S
Matches 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MANYSHAADNILQNLSP--LTAFLKLTSLGFIIGVSVVGNLLISILLVKDKTLHRAPYYF
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IAHHREYAKRMTLWTCAAVICMA-WTLSVAMAEPPVFDVGTYKFIREEDQCIFEHR-YFK 182

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A;Accession: JC7287
A;Molecule type: m&NA
A;Residuce: 1-375 <MAT>
A;Cross-references: UNIPROT:Q9NS67; UNIPARC:UPI0000049802; DDBJ:AB040799
C;Genetics:
                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revisio
C;Accession: I49246
R;Fishburn, C.S.; Carmon, S.; Fuchs,
FEBS Lett. 361, 215-219, 1995
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C; Keywords: brain; glyc
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C;Keywords: neurotransmitter receptor
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                                                                                                                                                                                                                                                                    A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                  D4 dopamine receptor - mouse
                                                                                                                                                                                                                                        A;Residues: 1-387 <RES>
                                                                                                                                                                                                                                                     A; Molecule type: DNA
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 74
                             65 CLADGIRSAVCEPEVLASVRHGSSWTESALSCKIVAFMAVLECEHAAFMLECISVTRYMA
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                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EHRYFKANDTLGFMLMLAVLMAATHAVYGKLLLFEYRHRKMKPVQMVPAISQNWTFHGPG
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 AAADLLLAVLVLPLFVYSEVQGGVWLLSPRLCDTLMAMDVMLCTASIFNLCAISVDRFVA
                                                               PESIGTGAGIGGAGAAALVGGVLLIGIV----LAGNSIVCVSVASERTIQTPTNYFIVSI
                                                                                             PEEV-SGA-LSPPSASAYV-KLVLLGLIMCVSLAGNAILSLLVLKERALHKAPYYFLLDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLDLCLADGLRALACLPAVMLAARRAAAAAGAPPGALGCKULAFLAALFCFHAAFLLLGV
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                                                                                                                                                                                                                                                                                                                                                                                 #sequence_revision 02-Jul-1996 #text_change
                                                                                                                                           13.3%;
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Pred.
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Pred. No. 1.6e-86;
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NO. 2.2e-16;
156
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G01977
d3 dopamine receptor - human
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C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: G08971
A; Accession: G01977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: G01977
R;Fishburn, C.S.; Park, B.
submitted to the EMBL Data Library, July 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
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Best Local S
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                                                                                                                                                                                                                                                       LSPDPAHLELKRYYSICQDTALGGPGFQERGGELKREEKTRNSLSPTIAPKLSLEVRKLS 302
                                                                                                                                                                                                                                                                                                                                                                YFKA-NDTLGFMLMLAVLMAATHAVYGKL-LLFEYRHRK------MKP-----
                                                                                                                                                                                                                                                                                                                                                                                                  TAVVMPVHYQHGTGQSSCRRVALMITAVWVLAFAVSCPLLFGFNT---TGDPTVCSISNP
                                                                                                                                                                                                                                                                                                                                                                                                                                   MAI---AHHREYAKRMTLWTCAAVICMAWTLSVAMAFPPVFDVGTYKFIREEDQCIFEHR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLAVADLL VATL VMPWVVYLEVTGGVWNFSRICCDVFVTLDVMMCTASILNLCAISIDRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLCLADGIRSAVCFPFVLASVRHGSSWTFSALSCKIVAFMAVLFCFHAAFMLFCISVTRY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYTCGAENSTGA-SQARPHAYYALSYCALILAI-VFGNGLVCMAVLKERALQTTTNYLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTTGEPEEVSGALSPPSASAYVKLVLLGLIMCVSLAGNAILSLLVLKERALHKAPYYFLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PQPPEPSSRRRRGAKITGRERKAMRVLPVVVGAFLVCWTPFFVVHITRALCPACFVSPRL 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPP----VSDPTQGPFFPDCPPPLPSLRTSPSDSSRPESELSQRPCSPGCLLADAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGQAAANWIAGFGRGPM----PPTLLGIR-----
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                                                                                                            ELYSAT-TWLGYVNSALNPVIYTTFNIEFRKAFLKILSC
                                                                                                                                              HRYLATAVWMSFAQAAVNPIVCFLLNKDLKKCLTTHAPC 357
                                                                                                                                                                                NGRLSTSLKLGPLOPRGVPLREKKATOMVAIVLGAFIVCWLPFFLTHVLNTHCQTCHVSP
                                                                                                                                                                                                                 NGHAASRRLLGMDEVKG----EKQLGRMFYAITLLFLLLWSPYIVACYWRVFVKACAV-P
                                                                                                                                                                                                                                                                                       -----VQMVPAISQNWTFHGPGATGQAAANWIAGFGRGPMPPTL-----LGIRQ--
                                                                                                                                                                                                                                                                                                                            DFVIYSSVVSFYLPFGV----TVLVYARIYVVLKQRRRKRILTRQNSQCNSVRPGFPQQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LATAVWMSFAQAAVNPIVCFLLNKDLK 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
2 - rat
5-hydroxytryptamine receptor 2 (5-HTR2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.1%; Score 260; DB 2; I
23.6%; Pred. No. 5.3e-16;
ative 71; Mismatches 180;
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C; Accession: S11280

C; Accession: S11280

C; Accession: S11280

R; Chambard, J.C.; van Obberghen-Schilling, E.; Haslam, R.J.; Vouret, V.; Pouyssegur, Nucleic Acids Res. 18, 5282, 1990

A; Title: Chinese hamster serotonin (5-HT) type 2 receptor cDNA sequence.

A; Reference number: S11280; MUID:90384833; PMID:2402449

A; Accession: S11280

A; Accession: S11280

A; Status: preliminary; translation not shown

A; Molecule type: mRNA

A; Molecule type: mRNA

A; Residues: 1-471 < CHA>

A; Cross-references: UNIPROT:P18599; UNIPARC:UPI0000124F2E; EMBL:X53791; NID:g49455; EC; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
S11280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    serotonin receptor 2 - Chinese hamster
N;Alternate names: 5-hydroxytryptamine receptor 2 (5-HTR2)
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-449 < PRI>
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A;Accession: S02011
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C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S02011
R;Pritchett, D.B.; Bach, A.W.J.; Wozny, M.; Taleb, O.; Dal Toso, R.; Shih,
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Matches 86
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PPTCLSILHLQEKNWSALLTAVVIILTIAGNILVIMAVSLEKKLQNATNYFLMSLAIADM 121
                                            PPSASAYVKL-----VLLGLIMCVSLAGNAILSLLVLKERALHKAPYYFLLDLCLADG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLLFLLLWSPYIVACYWRVFVK-AC--AVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLK 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NDTLGFMLMLAVLMAATHAVYGKLLLFE-----YRHRKMKPVQMVP--AISQNWTFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HHSRFNSRTKAFLKIIAV----WTISVGISMPIPVFGLQDDSKVFKEGSCLLADDNFVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLGFLVMPVSMLTILYGYRWPLPSKLCAIWIYLDVLFSTASIMHLCAISLDRYVAIQNPI 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPSASAYVKL------VLLGLIMCVSLAGNAILSLLVLKERALHKAPYYFLLDLCLADG
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                                                                                                                 13.0%; Score 259.5; DB 2; 23.1%; Pred. No. 7e-16;
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Pred. No. 6.7e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----repgsyagrrtmosisneokackvigivff--
                                                                                                Mismatches
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                                                                                                152;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5-hydroxytryptamine 2 receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
C;Accession: S40689
R;Yang, W.; Chen, K.; Lan, N.C.; Gallaher, T.K.; Shih, J.C.
J. Neurosci. Res. 33, 196-204, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-471 <YAN>
A;Residues: 1-471 <YAN>
A;Cross-references: UNIPROT:P35363; UNIPARC:UPI00000040D4; EMBL:S49542; NID:g261074; PII
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NWTFHGPGA-TGQAAANWIAGFGRGPMPPTLLGIRQNGHAASRRLLGMDEVKGEKQLGRM
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                                                  --LFVVMWCPFFITNIMAVICKESCNENVIGALLNVFVWIGYLSSAVNPLVYTLFNKTYR
                                                                                                TLLFLLLWSPYIVACYWRVFVK-AC--AVPHRYLATAVWMSEAQAAVNPIVCFLLNKDLK 348
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KCLTTHAPC 357
                                                                                                                                                                                                     GPGATGQAAANWIAGFGRGPMPPTLLGIRQNGHAASRRLLG--MDEVKGEKQLGRMFYAI
                                                                                                                                                                                                                                                          GSFVAFFIPLTI-MVITYFLTIKSLQKEATLCVSDLSTRAKLSSFSFLPQSSLSSEKLF-
                                                                                                                                                                                                                                                                                                          NDTLGFMLMLAVLMAATHAVYGKLLLFE-----YRHRKMKPVQMVP--AISQNWTFH
                                                                                                                                                                                                                                                                                                                                                             HHSRFNSRTKAFLKIIAV----WTISVGISMPIPVFGLQDDSKVFKEGSCLLADDNFVLI
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                                                                                                                                                                                                                                                                                                                                                                                                        -HHRFYAKRMTLWTCAAVICMAWTLSVAMAFF-PVFDVGTYKFIREEDQCIF-EHRYFKA 183
                                                                                                                                                  ----QRSIH---
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24.1%; Pred. No. 7e-
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                                                                                                                                                        ------REPGSYAGRRTMQSISNEQKACKVLGIVFF--
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A;Introns: 1381; 2051
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor;
F;11-132/Domain: transmembrane #status predicted <TM1>
F;111-132/Domain: transmembrane #status predicted <TM3>
F;148-170/Domain: transmembrane #status predicted <TM4>
F;234-254/Domain: transmembrane #status predicted <TM5>
F;234-254/Domain: transmembrane #status predicted <TM6>
F;326-346/Domain: transmembrane #status predicted <TM7>
F;363-384/Domain: transmembrane #status predicted <TM7>
F;363-384/Domain: transmembrane #status predicted <TM7>
F;363-384/Domain: transmembrane #status predicted <TM7>
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A,Note: the authors translated the codon CCA for residue 405 as Thr and CCG for residue
A,Note: sequence extracted from NCBI backbone (NCBIN:110508, NCBIN:110524, NCBIN:110527)
R;Saltzman, A.G.; Morse, B.; Whitman, M.M.; Ivanshchenko, Y.; Jaye, M.; Felder, S.
Biochem. Biophys. Res. Commun. 181, 1469-1478, 1991
A;Title: Cloning of the human serotonin 5-HT2 and 5-HT1C receptor subtypes.
A;Reference number: JS0615; MUID:92109767; PMID:1722404
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Brain Res. Mol. Brain Res. 14, 20-26, 1992
A;Title: The human 5-HT2 receptor is encoded by a multiple intron-exon A;Reference number: A43956; MUID:92356792; PMID:1323014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Nolecule type: mRNA
A; Residues: 1-471 <RES>
A; Cross-references: UNIPARC: UPI000000126E;
A; Cross-references: UNIPARC: UPI000000126E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Neurochem. 63, 465-469, 1994
A;Title: Primary structure of the human platelet serotonin A;Reference number: I56514, MUID:94308772; PMID:8035173
A;Accession: I56514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPARC:UPI000000126E; R;Cook, E.H.
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A; Residues: 1-471 < CHE>
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993
C;Accession: A43956; JS0615; I56514
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                                                                                                                                                             119 ADMLLGFLVMPVSMLTILYGYRWPLPSKLCAVWIYLDVLFSTASIMHLCAISLDRYVAIQ 178
        181
                                                                                                                                                                                                          67 ADGIRSAVCEPEVLASVRHGSSWTESALSCKIVAEMAVLECEHAAEMLECISVTRYMAIA 126
                                                                                                                                                                                                                                                                                                                     13 GALSPPSASAY-----VKLVLLGLIMCVSLAGNAILSLLVLKERALHKAPYYFLLDLCL
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                             NPIHHSRFNSRTKAFLKIIAV--
                                                                                                          ----HHRFYAKRMTLWTCAAVICMAWTLSVAMAFP-PVFDVGTYKFIREEDQCIF-EHRY 180
        FKANDTLGFMLMLAVLMAATHAVYGKLLLFEY---
                                                                                                                                                                                                                                                                  GCLSPSCLSLLHLQEKNWSALLITAVVIILTIÄGNILVIMAVSLEKKLQNATNYFLMSLAI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2A - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDB:125192; OMIM:182135
                                                                                                                                                                                                                                                                                                                                                                                                12.9%;
                                                                                                                                                                                                                                                                                                                                                                          63;
                                                                                                                                                                                                                                                                                                                                                                                                Score 257; DB 2;
Pred. No. 1.2e-15;
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                WIISVGISMPIPVFGLQDDSKVFKEGSCLLADDNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:S71229; NID:g547295; PIDN:AAB31320.1; vascular contraction and platelet aggregation
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 471;
                -RHRKMKPVQMVPAIS----
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A;Cross-references: UNIPROT:P14842; UNIPARC:UPI00001778DF; GB:M30705 R;Liu, J.; Chen, Y.; Kozak, C.A.; Yu, L. Genomics II, 231-234, 1991 Genomics II, 231-234, 1991 A;Title: The 5-HTZ serotonin receptor gene Htr-2 is tightly linked the A;Reference number: A40574; MUID:92112222; PMID:1765383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           serotonin receptor 2 - rat
N;Alternate names: 5-hydroxytryptamine receptor 2 (5-HTR2)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan:1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: A;486; A40574
R;Julius, D.; Huang, K.N; Livelli, T.J.; Axel, R.; Jessell, T.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 928-932, 1990
A;Title: The SHT2 receptor defines a family of structurally distinct but fur A;Reference number: A;4863; MUID:90138991; PMID:2300586
A;Accession: A;4863
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C;Keywords: G protein-coupled receptor;
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A; Residues: 1-309, 'R', 311-471 <LIU>
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A; Residues: 1-471 < JUL>
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                                                                                                            TLLFLLLWSPYIVACYWRVFVK-AC--AVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLK 348
                                                                                                                                                                                      GPGATGQAAANWIAGFGRGPMPPTLLGIRQNGHAASRRLLG--MDEVKGEKQLGRMFYAI
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SAFSRYIQC
                                    KCLTTHAPC
                                                                     -; LFVVMMCPFFITNIMAVICKESCNENVIGALLNVFVWIGYLSSAVNPLVYTLFNKTYR
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                                                                                                                                                                                                                                                               NDTLGFMLMLAVLMAATHAVYGKLLLFE-----YRHRKMKPVQMVP--AISQNWTFH
                                                                                                                                                                                                                                                                                                  HHSRFNSRTKAFLKIIAV----WTISVGISMPIPVFGLQDDSKVFKEGSCLLADDNFVLI
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                                                                                                                                                 ----QRSIH----
                                                                                                                                                                                                                                                                                                                                                                                                             IRSAVCFPFVLASVRHGSSWTFSALSCKIVAFMAVLFCFHAAFMLFCISVTRYMAIA---
                                                                                                                                                                                                                                                                                                                                   HHRFYAKRMTLWTCAAVICMAWTLSVAMAFP-PVFDVGTYKFIREEDOCIF-EHRYFKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 256.5; DB 2;
Pred. No. 1.3e-15;
9; Mismatches 150;
                                                                                                                                                 ---REPGSYAGRKTMQSISNEQKACKVLGIVFF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycoprotein;
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R;Kopin, A.S.; Lee, Y.M.; McBride, B.W.; Miller, L.J.; l
Proc. Natl. Acad. Sci. U.S.A. 89, 3605-3609, 1992
A;Title: Expression cloning and characterization of the
A;Reference number: S32817; MUID:92228835; PMID:1373504
A;Accession: S32917
                                                                                                                                                                                                                                                                                                                                                                          RESULT
S32817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D3 dopamine receptor - green monkey
C;Speciaes: Cercopithecus aethiops (green monkey, grivet)
C;Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text
C;Accession: G00013
R;Ross, P.C.
                                                                                                                                                                                                                                                                                          gastrin receptor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S32817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, A;Reference number: G00049
A;Accession: G00013
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C;Keywords: neurotransmitter receptor
                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-453 < KOP>
                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
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                                                                                                                A; Cross-references: UNIPROT: P30552; UNIPARC: UPI000012B0E8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P52703; UNIPARC:UPI0000128DB0;
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                                                                         ;Superfamily: neurokinin 1 receptor; transmembrane;Keywords: G protein-coupled receptor; transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 TAVVMPVHYQHGTGQSSCRRVTL----MITAVWVLAFAVSCPLLFGFNT---TGDPTVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFEHRYFKA-NDTLGFMLMLAVLMAATHAVYGKL-LLFEYRHRK-------MKP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHVSPELYSAT-TWLGYVNSALNPVIYTTFNIEFRKAFLKILSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAV-PHRYLATAVWMSFAQAAVNPIVCFLLNKDLKKCLTTHAPC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRKLSNGRLSTSLKLGPLQPRGVPLREKKATQMVAIVLGAFIVCWLPFFLTHVLNTHCQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SISNPDFVIYSSVVSFYLPFGV----TVLVYARIYVVLKORRRKRILTRONSOCNSVRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLAVADILVATIVMEWVVYLEVTGGVWNESRVCCDVFVTLDVMMCTASILNICAISIDRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69;
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Pred.
Score 250.5; DB 2;
Pred. No. 4.5e-15;
1; Mismatches 171;
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No. 1.2e-15;
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                                                                                                                                                                                                                                                                          M.; Lin, H.Y.; Kolakowski
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A;Gene: GDB:DRD4
A;Map position: 11p15.5-11p15.5
A;Map position: 11p15.5-11p15.5
A;Introns: 95/3; 133/2; 269/2; 321/1
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; gly(F;34-60/Domain: transmembrane #status predicted <TM1>F;34-60/Domain: transmembrane #status predicted <TM3>F;153-174/Domain: transmembrane #status predicted <TM3>F;153-174/Domain: transmembrane #status predicted <TM4>F;193-214/Domain: transmembrane #status predicted <TM5>F;315-319/Domain: transmembrane #status predicted <TM5>F;315-339/Domain: transmembrane #status predicted <TM6>F;349-368/Domain: transmembrane #status predicted <TM6-F;349-368/Domain: transmembrane #status predicted <TM6-F;349-368/Domain: transmembrane #status predicted <TM6-F;349-368/Domain: trans
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C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: S15079
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DYHUD4
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A;Title: Cloning of the gene for a human dopamine D(4) receptor with high affinit A;Reference number: S15079; MUID:91204054; PMID:1840645
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A; Residues: 1-387 < VAN>
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C;Genetics:
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Best Local S
Matches 88
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   CLADGIRSAVCFPFVLASVRHGSSWTFSALSCKIVAFMAVLFCFHAAFMLFCISVTRYMA
                                                          GASAGASAGLAGQGAAALVGGVLLIGAV----LAGNSLVCVSVATERALQTPTNSFIVSL
                                                                                                                    GEPEEVSGALSPPSASAYV-KLVLLGLIMCVSLAGNAILSLLVLKERALHKAPYYFLLDL
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                                                                                                                                                                                 61; Mismatches 183;
                                                                                                                                                                                                             Score 247.5; DB 1
Pred. No. 7.1e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gastrin/cholecystokinin B receptor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: JC2459
C;Accession: JC2459
Biochem. Biophys. Res. Commun. 202, 947-953, 1994
A;Title: Molecular cloning and structural analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning and structural analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning and structural analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning and structural analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning and structural analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning and structural analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning and structural analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning and structural analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning and structural analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning and structural analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning and structural analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning and structural analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning and structural analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning and structural analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning and structural analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning analysis of the rabbit gastrin/CCKB receptor (A;Title: Molecular Cloning analysis of the rabbit
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                                                                   232 FHGPGATGQAAANW--
                                                                                                                                                                                                                                                                                                         123
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                                                                                                                                                                                                                                                                                                                                                                                                                             DLCLADGIRSAVCFPFVLASVRHGSSWTFSALSCKIVAFMAVLFCFHAAFMLFCISVTRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IA----HHRFYAKRMTLWTCAAVICMAWTLSVAMAFPPVFDVGTYKFIREEDQCIFEHR- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NTTGEPEEVSGALSPPSASAYVKLVLLGLIMCVSLAGNAILSLLVLKERALHKAPYYFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VFNAEFR 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLNKDLK 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KQLGRMFYAITLLFLLLWSPYIVACYWRVFVKACAVPHRYLATAVWMSFAQAAVNPIVCF 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSGPGPPSPTPPAP
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            LPGGAAPGPVHQNGRCRPEAGLAGEDGDGCYVQLPRSRPALELSALTAPISGPGPGPRP-
                                                                                                                             WPSARVRQTWSVLLLLLLFFVPGVVMAVAYGLISRELYLGLRFDSDSDSESQSRVRGQGG
                                                                                                                                                                                 HRYFKANDTLGFMLML-----AVLMAATHAVYGKLLLFEYRHRKMKPVQMVPAISQNWT
                                                                                                                                                                                                                                               SAICRPLQARVWQTRSHAARVILATWLLSGLLMVPYPVYTAVQPVGPRVL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 247; DB 2; I
Pred. No. 9.3e-15;
3; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----KPVQMVP
                                                                      ----IAGFGRGPMPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86;
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                                                                                                                                                                                                                                                     -QCVHR
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PIDN

| Search completed:<br>Job time : 42 sec | B &               | B &  | Qy<br>bb  | Qy<br>Db   | Qy<br>Db   | g 2°   | da<br>Q  | Query Match<br>Best Local S<br>Matches 82   | Qy 257 TLLGIRG OF TLLGIRG OF TLLGIRG OF THE TLLGIRG OF THE TLLGIRG OF TLLGIRG |
|--|-------------------|--|---|--|--|--|--|---|--|
| omplet<br>: 42                         | 345<br>392        | 288<br>332   | 243<br>275  | 183<br>245   | 125<br>187   | 65<br>127  | 8<br>67  | Match<br>ocal S<br>s 82   | 326 327 TL 326 317 VP 317 VP 319 5 5   |
| ed: March 7, 2006, 12:54:58<br>secs    | KDLKKCLTTHAPC 357 | FYAITLLFLLLWSPYIVACYWRVFVKACA-VPHRYLATAVWMSFAQAAVNPIVCFLLN 344 | ANWIAGFGRGPMPPTLLGIRONGHAASRRLLGMDEVKGEKQLGRM 287 | ANDTLGFMLMLAVLMAATHAVYGKLLLFEYRHRKMKPVQMVPAISQNWTFHGPGATGQAA 242 | IAHHREYAKRMTLMTCAAVICMAWTLSVAMAFPPVFDVGTYKFIREEDQCIFEHRYFK 182 | CLADGIRSAVCFPFVLASVRHGSSWTFSALSCKIVAFMAVLFCFHAAFMLFCISVTRYMA 124 | PEEVSGALSPPSASAYVKLVLIGLIMCVSLAGNAILSLLVLKERALHKAPYYFLLDL 64 | 12.2%; Score 244; DB 2; Length 448;<br>Similarity 22.0%; Pred. No. 1.7e-14;<br>Conservative 66; Mismatches 167; Indels 58; Gaps 10; | Qy  257 TLLGIRQNGHAASRRLLGWDEVKGEKQLGRMFYAITLLFLLLWSPYIVACYWRVFVKACA 316   |

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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::
                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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             GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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Sequence 68, Appl
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| 4.                | 44                | 43                | 42                | 41                | 40                | 39                | 38               | 37                | 36                | 35                | 34                | 33               | 32                 | 31                | 30                | 29                | 28                |
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| 379               | 370               | 370               | 370               | 370               | 370               | 370               | 370              | 370               | 370               | 370               | 370               | 370              | 370                | 370               | 370               | 370               | 370               |
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| US-10-073-885-79  | US-10-723-955-28  | US-10-898-329-24  | US-10-898-329-4   | US-10-788-197-67  | US-10-755-889-6   | US-10-782-596-26  | US-10-723-955-28 | US-10-692-605-14  | US-10-292-798-886 | US-10-417-820A-28 | US-10-393-807-26  | US-10-272-983-26 | US-10-225-567A-611 | US-10-318-142-24  | US-10-318-142-4   | US-10-165-844-7   | US-10-043-945-2   |
| Sequence 79, Appl | Sequence 28, Appl | Sequence 24, Appl | Sequence 4, Appli | Sequence 67, Appl | Sequence 6, Appli | Sequence 26, Appl |                  | Sequence 14, Appl | Sequence 886, App | •                 | Sequence 26, Appl | •                | Sequence 611, App  | Sequence 24, Appl | Sequence 4, Appli | Sequence 7, Appli | Sequence 2, Appli |

ALIGNMENTS

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APPLICANT: Dang, Huong T.
APPLICANT: Chen, Ruoping
APPLICANT: Chen, Ruoping
APPLICANT: Chen W.
TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G PJ
FILE REFERENCE: AREN-0054
CURRENT APPLICATION NUMBER: US/09/876,252
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 09/10,060
PRIOR FILING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/121,852
PRIOR APPLICATION NUMBER: 60/121,852
PRIOR APPLICATION NUMBER: 60/121,852
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; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
; PRIOR FILING DATE: 1999-10-01
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US-09-876-252-22
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APPLICANT: Lehmann
APPLICANT: Chalmer
APPLICANT: Lowitz
APPLICANT: Lin, I
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Best Local
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ORGANISM: Homo sapiens
-09-875-076-20
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373; Conservative 0
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Chalmers, Derek T.
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Pred. No. 5e-189;
Mismatches 0
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; LENGTH: 373
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; ORGANISM: Homo :
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SOFTWARE: Pate
SEQ ID NO 22
FRIGHT: 373
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Best Local Similarity 100.0%; Pred. No. 5e-189;
Matches 373; Conservative 0; Mismatches 0
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DR APPLICATION NUMBER: 60/123,944
DR FILING DATE: 1999-03-12
DR PPLICATION NUMBER: 60/123,945
DR FILING DATE: 1999-03-12
DR APPLICATION NUMBER: 60/123,948
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DR FILLING DATE: 1999-05-28
PR FILLING DATE: 1999-05-28
DR FILLING DATE: 1999-05-28
DR APPLICATION NUMBER: 60/137,127
DR FILING DATE: 1999-05-28
DR FILING DATE: 1999-05-28
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FILING DATE: 1999-05-28
APPLICATION NUMBER: 60/141,448
FILING DATE: 1999-06-29
APPLICATION NUMBER: 60/136,437
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APPLICATION NUMBER: 60/151,114
FILING DATE: 1999-08-27
APPLICATION NUMBER: 60/108,029
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FILING DATE: 1999-03-12
APPLICATION NUMBER: 60/
FILING DATE: 1999-03-12
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APPLICATION NUMBER: 60/157,281
FILING DATE: 1999-10-01
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FILING DATE: 1999-09-29
APPLICATION NUMBER: 60/156,653
FILING DATE: 1999-09-29
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APPLICATION NUMBER: 60/156,555
FILING DATE: 1999-09-29
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APPLICATION NUMBER: 60/136,436
FILING DATE: 1999-05-28
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APPLICATION NUMBER: 60/156,633
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              121 RYMAIAHHRFYAKRMTLWTCAAVICMAWTLSVAMAFPPVFDVGTYKFIREEDQCIFEHRY
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MANTTGEPEEVSGALSPPSASAYVKLVLLGLIMCVSLAGNAILSLLVLKERALHKAPYYF
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373; 0;

Gaps

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; Remaining prior Application data removed -
NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIN Ver. 2.1
; SEQ ID NO 20
LENGTH: 373
TYPE: PRT
ORGANISM: Homo sapiens
US-10-272-983-20
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US-10-272-983-20
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CURRENT APPLICATION NUMBER: US/10/272,983
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US/09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/120,416
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Best Local S:
Matches 373
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APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/136,567 PRIOR FILING DATE: 1999-05-28
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FILING DATE: 1999-05-28
APPLICATION NUMBER: 60/136,437
FILING DATE: 1999-05-28
APPLICATION NUMBER: 60/136,439
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APPLICATION NUMBER: 60/121,851
FILING DATE: 1999-02-26
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121 RYMAIAHHRFYAKRMTLWTCAAVICMAWTLSVAMAFPPVFDVGTYKFIREEDQCIFEHRY 180
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373; Conserv
                                      61;LLDLCLADGIRSAVCFPFVLASVRHGSSWTFSALSCKIVAFMAVLFCFHAAFMLFCISVT
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US-10-393-807-20
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CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: US/09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR APPLICATION NUMBER: 60/133,949
PRIOR APPLICATION NUMBER: 60/136,436
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SEQ ID NO 20
LENGTH: 373
TYPE: PRT
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                                                                                                                                                                                                                         Query Match
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APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
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APPLICATION NUMBER: 60/136,437
FILING DATE: 1999-05-28
APPLICATION NUMBER: 60/136,439
FILING DATE: 1999-05-28
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  LLDLCLADGIRSAVCFPFVLASVRHGSSWTFSALSCKIVAFMAVLFCFHAAFMLFCISVT
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Best Local S
Matches 373
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NUMBER OF SEQ ID NOS: 155
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 373
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PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-11-27
PRIOR FILING DATE: 1998-11-27
PRIOR FILING DATE: 1998-11-27
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                                                                                                                                 TYPE: PRT
ORGANISM: Homo
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APPLICATION NUMBER: 60/109,213
FILING DATE: 1998-11-20
APPLICATION NUMBER: 60/123,944
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No. US20030229216A1
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                                                       Score 1992; DB 4;
Pred. No. 5e-189;
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TITIE OF INVENTION: Constitutively Activated Human G F
TITIES OF INVENTION: Receptors
FILE REFERENCE: 7.US29.CON
CURRENT APPLICATION NUMBER: US/10/723,955
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 10/417,820
PRIOR FILING DATE: 2003-4-16
PRIOR PILING DATE: 1999-10-12
PRIOR PILING DATE: 1999-10-12
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 09/110,060
PRIOR FILING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR FILING DATE: 1999-02-26
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PRIOR APPLICATION NUMBER: 60/110,060
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PRIOR APPLICATION NUMBER: 60/123,944
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,945
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,948
PRIOR FILING DATE: 1999-03-12
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Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 148 SOFTWARE: Patentin version 3.2 SEQ ID NO 22 LENGTH: 373 TYPE: PRT ORGANISM: Homo sapiens
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Chen, Ruoping
Gore, Martin
White, Carol
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No. US20040110238A1
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Lowitz, Kevin P.
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APPLICANT: Liaw, Chen W.

APPLICANT: Liaw, Chen W.

APPLICANT: Liin, I Liin

APPLICANT: Liin, I Liin

FILE OF INVENTION: Human Orphan G Protein Coupled Receptors

FILE REFERENCE: AREN0050

CURRENT APPLICATION NUMBER: US/10/782,596

CURRENT PILING DATE: 2001-06-06

PRIOR APPLICATION NUMBER: US/9/875,076

PRIOR FILING DATE: 1999-10-12

PRIOR APPLICATION NUMBER: 60/120,416

PRIOR APPLICATION NUMBER: 60/120,416

PRIOR FILING DATE: 1999-02-16

PRIOR APPLICATION NUMBER: 60/121,851

PRIOR APPLICATION NUMBER: 60/121,851

PRIOR APPLICATION NUMBER: 60/123,946

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,946

PRIOR APPLICATION NUMBER: 60/123,949

PRIOR APPLICATION NUMBER: 60/136,436

PRIOR APPLICATION NUMBER: 60/136,436

PRIOR APPLICATION NUMBER: 60/136,437

PRIOR PILING DATE: 1999-05-28

PRIOR PILING DATE: 1999-05-28
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Publication No. US20040137509A1
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Dang, Huong T.
Remaining Prior Application
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 373
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TITLE OF INVENTION: CONSTITUTIONS ACTIVATED HUM
TITLE OF INVENTION: Receptors
FILE REFERENCE: 7.US29.CON
CURRENT APPLICATION NUMBER: US/10/723,955
CURRENT FILING DATE: 2003-11-26
PRIOR PILLING DATE: 2003-416
PRIOR PILLING DATE: 2003-416
PRIOR PILLING DATE: 1999-10-12
PRIOR PILLING DATE: 1999-10-12
PRIOR PILLING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR FILLING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR FILLING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR PILLING DATE: 1999-02-16
PRIOR PILLING DATE: 1999-02-16
PRIOR PILLING DATE: 1999-02-26
PRIOR PILLING DATE: 1999-02-30
PRIOR PILLING DATE: 1998-11-20
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APPLICANT: Behan, Do
APPLICANT: Chalmers
APPLICANT: Lin, I-L
APPLICANT: Liaw, Ch
APPLICANT: Lehman-B
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APPLICATION NUMBER: 60/109,213
FILING DATE: 1998-11-20
APPLICATION NUMBER: 60/123,944
FILING DATE: 1999-03-12

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TITLE OF INVENTION: A novel G protein coupled recepter protein FILE REFERENCE: Y9905
CURRENT APPLICATION NUMBER: US/10/318,142
CURRENT FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: US/09/622,439
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: JP P1998-060245
PRIOR APPLICATION NUMBER: JP P1998-060245
PRIOR APPLICATION NUMBER: JP P1999-026774
PRIOR FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: JP P1999-026774
PRIOR APPLICATION NUMBER: JP P1999-
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PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,948
PRIOR FILING DATE: 1999-03-12
Remaining Prior Application data removed - See File Wrapper or NUMBER OF SEQ ID NOS: 148
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
SEQ ID NO 22
LENGTH: 373
TYPE: PRT
ORGANIUM: Homo sapiens
US-10-723-955-22
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Publication No. US20030077662A1
GENERAL INFORMATION:
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Matches 373; Conserv
Query Match
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GENERAL INFORMATION:

APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.

APPLICANT: Brown, Joseph P.

APPLICANT: Brown, Joseph P.

APPLICANT: Roush, Christine L.

APPLICANT: Roush, Christine L.

FILE REFERENCE: 1920-4-4

CURRENT APPLICATION NUMBER: US/10/225,567A

CURRENT APPLICATION NUMBER: 40/257,144

PRIOR PILING DATE: 2001-12-19

PRIOR APPLICATION WIMBER: 60/257,144

PRIOR PILING DATE: 2000-12-19

NUMBER OF SEQ ID NOS: 2292

SOFTWARE: Patentin version 3.1

SEQ ID NO 615
                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens 
US-10-225-567A-615
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o. US20030113798A1
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Pred. No. 2e-188;
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SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 59
LENGTH: 37
TYPE: PRT |
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2004-02-26
PRIOR APPLICATION NUMBER: PCT/US03/14581
PRIOR FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: 60/379,986
PRIOR APPLICATION NUMBER: 60/379,986
PRIOR APPLICATION NUMBER: 60/401,698
PRIOR PPLICATION NUMBER: 60/401,698
PRIOR PILING DATE: 2002-08-07
NUMBER OF SEQ ID NOS: 94
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Publication No. US20050032125A1

GENERAL INFORMATION:
APPLICANT: OAKLEY, ROBERT H.
APPLICANT: HUDSON, CHRISTINE C.
TITLE OF INVENTION: CONSTITUTIVELY TRANSLOCATING
FILE REFERENCE: NRK. 108
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Best Local Similarity
Matches 372; Conserv
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Pred. No. 2e-188;
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Sequence 77, Application US/10073885

Publication No. US20030096346A1

GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, an FILE REFERENCE: PJZ03C1
CURRENT APPLICATION NUMBER: US/10/073,885
CURRENT FILING DATE: 2002-02-14
Prior Application removed - See file Wrapper or NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 77
LENGTH: 378
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Publication No. US20050042683A1

GENERAL INFORMATION:
APPLICANT: Yamanouchi Pharmceutical Co., Lt
TITLE OF INVERTION: A novel G protein couple
FILE REFERENCE: Y9905
CURRENT APPLICATION NUMBER: US/10/898,329
CURRENT FILING DATE: 2004-07-26
PRIOR APPLICATION NUMBER: US/10/318,142
PRIOR PILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: US/09/622,439
PRIOR PILING DATE: 2000-08-17
PRIOR PILING DATE: 2000-08-17
PRIOR PILING DATE: 1998-03-12
PRIOR PILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 2e-188;
0; Mismatches 1;
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Sequence 61, Application US/10788197

| Sequence 61, Application US/10788197
| Publication No. US20050032125A1
| GENERAL INFORMATION:
| APPLICANT: OAKLEY, ROBERT H.
| APPLICANT: HUDSON, CHRISTINE C.
| TITLE OF INVENTION: CONSTITUTIVELY TRANSLOCATING CELL LINIFILE REFERENCE: NRX.108
| CURRENT APPLICATION NUMBER: US/10/788,197
| CURRENT APPLICATION NUMBER: PCT/US03/14581
| PRIOR APPLICATION NUMBER: PCT/US03/14581
| PRIOR APPLICATION NUMBER: 60/379,986
| PRIOR FILING DATE: 2003-05-12
| PRIOR FILING DATE: 2002-05-13
| PRIOR FILING DATE: 2002-05-13
| PRIOR FILING DATE: 2002-08-07
| NUMBER: OF SEQ ID NOS: 94
| SOFTWARE: PATENTIN VET. 3.2
| SEQ ID NO 61
| LENGTH: 387
| TYPE: PRT
| ORGANISM: Homo sapiens
| US-10-788-197-61
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Best Local Similarity 99.7
Matches 372; Conservative
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Matches 372; Conserv
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Pred. No. 2.1e-188;
Pred. No. 2.1e-188;
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APPLICANT: Takeda Chemical Industries, Ltd.

TITLE OF INVENTION: Determination of a ligand

FILE REFERENCE: P03-0006PCT

CURRENT APPLICATION NUMBER: US/10/505,486

CURRENT FILING DATE: 2004-08-20

PRIOR APPLICATION NUMBER: JP 2002-45728

PRIOR APPLICATION NUMBER: JP 2002-45728

PRIOR APPLICATION NUMBER: JP 2002-213949

PRIOR APPLICATION NUMBER: JP 2002-213949

PRIOR APPLICATION NUMBER: JP 2002-2337

PRIOR APPLICATION NUMBER: JP 2002-298237

PRIOR APPLICATION NUMBER: JP 2002-298237

PRIOR FILING DATE: 2002-10-11

NUMBER OF SEQ ID NOS: 233

SEQ ID NO 49
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US-10-505-486-49
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Best Local Similarity 99.7%;
Matches 372; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 611
TYPE: PRT
ORGANISM: Human
                                                 301
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GGAPAPREPYCVM 373
                           PYIVACYWRVEVKACAVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLKKCLRTHAPCWGT
                                           PYIVACYWRVFVKACAVPHRYLATAVWNSFAQAAVNFIVCFLLNKDLKKCLTTHAPCWGT
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                                                                                                                                          FKANDTLGFMLMLAVLMAATHAVYGKLLLFEYRHRKMKPVQMVPAISQNWTFHGPGATGQ
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                                                                                                                                                                                                                                                                                                                                                                                  Score 1986; DB 5;
Pred. No. 3.6e-188;
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Db 361 GGAPAPREPYCVM 373

Search completed: March 7, 2006, 12:58:41
Job time: 167 secs

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Maximum Match 100%
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Maximum DB seq length: 200000000
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1: /cgn2 6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

2: /cgn2-6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

4: /cgn2-6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

5: /cgn2-6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

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US-11-040-218-73
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US-11-115-564-3
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Sequence 12, Appl
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Sequence 14, Appl
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Sequence 248, App
Sequence 340, Appl
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| 9.8               | 9.8               | 9.8               | 9.8               | 9.8               | 9.8               | 9.8               | 9.8               | 9.9              | 9.9               | 9.9               | 9.9               | 10.0              | 10.1              | 10.2              | 10.3              | 10.3              | 10.4              | 10.4              | 10.5              |
| 446               | 338               | 338               | 338               | 259               | 259               | 259               | 259               | 347              | 347               | 400               | 415               | 353               | 269               | 440               | 348               | 348               | 350               | 442               | 389               |
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| Sequence 67, Appl | Sequence 82, Appl | Sequence 63, Appl | Sequence 175, App | Sequence 29, Appl | Sequence 27, Appl | Sequence 237, App |                   |                  | Sequence 57, Appl | Sequence 55, Appl | Sequence 2, Appli | Sequence 9, Appli | Sequence 5, Appli | Sequence 2, Appli | Sequence 34, Appl | Sequence 48, Appl | Sequence 546, App | Sequence 34, Appl | Sequence 837, App |

ALIGNMENTS

## APPLICANT: OMALEY, ROBERT H. APPLICANT: HUDSON, CHRISTINE C. TITLE OF INVENTION: CONSTITUTIVELY TRANSLOCATING CEL FILE REFERENCE: NRK.108 CURRENT APPLICATION NUMBER: US/11/040,218 CURRENT FILING DATE: 2005-01-21 PRIOR APPLICATION NUMBER: US/10/788,197 PRIOR FILING DATE: 2004-02-26 PRIOR FILING DATE: 2004-02-26 PRIOR FILING DATE: 2003-05-12 PRIOR APPLICATION NUMBER: E07/US03/14581 PRIOR APPLICATION NUMBER: 60/379,986 PRIOR APPLICATION NUMBER: 60/379,986 PRIOR APPLICATION NUMBER: 60/401,698 PRIOR FILING DATE: 2002-08-07 NUMBER OF SEQ ID NOS: 94 S 밁 S 밁 á 망 밁 S US-11-040-218-59 US-11-040-218-59 SOFTWARE: Pat SEQ ID NO 59 LENGTH: 373 Sequence 59, Application US/11040218 Publication No. US20060029983A1 GENERAL INFORMATION: Query Match Best Local Similarity Matches 372; Conserv TYPE: PRT ORGANISM: Homo sapiens 181 121 121 RYMAIAHRFYAKRMTLWTCAAVICMAWTLSVAMAFPPVFDVGTYKFIRBEDQCIFEHRY 61 61 PatentIn Ver. 3.2 LLDLCLADGIRSAVCFPFVLASVRHGSSWTFSALSCKIVAFMAVLFCFHAAFMLFCISVT MANTTGBPBEVSGALSPPSASAYVKLVLLGLIMCVSLAGNAILSLLVLKERALHKAPYYF FKANDTLGFMLMLAVLMAATHAVYGKLLLFEYRHRKMKFVQMVFAISQNWTFHGFGATGQ LLDLCLADGIRSAVCFPFVLASVRHGSSWTFSALSCKIVAFMAVLFCFHAAFMLFCISVT MANTTGEPEEVSGALSPPSASAYVKLVLLGLIMCVSLAGNAILSLLVLKERALHKAPYYF RYMAIAHHRFYAKRMTLWTCAAVICMAWTLSVAMAFPPVFDVGTYKFIREEDQCIFEHRY 99.7%; ilarity 99.7%; Conservative ( 0 Score 1986; DB 7; Length 373; Pred. No. 1e-184; O; Mismatches 1; Indels CELL <u>,,</u>

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PRIOR APPLICATION NUMBER: 60/401,698
PRIOR FILING DATE: 2002-08-07
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 61
LENGTH: 387
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 61, Application US/110 Publication No. US20060029983A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.7%;
Best Local Similarity 99.7%;
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APPLICANT: HUDSON, CHRISTINE C.
TITLE OF INVENTION: CONSTITUTIVELY TRANSLOCATING CELL LINE
FILE REFERENCE: NRK.108
CURRENT APPLICATION NUMBER: US/11/040,218
CURRENT FILING DATE: 2005-01-21
PRIOR APPLICATION NUMBER: US/10/788,197
PRIOR FILING DATE: 2004-02-26
PRIOR APPLICATION NUMBER: PCT/US03/14581
PRIOR APPLICATION NUMBER: PCT/US03/14581
PRIOR APPLICATION NUMBER: 60/379,986
PRIOR APPLICATION NUMBER: 60/379,986
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RESULT 4
US-11-040-218-65
US-11-040-218-65
Sequence 65, Application US/11040218
Publication No. US20060029983A1
GENERAL INFORMATION:
APPLICANT: HUDSON, CHRISTINE C.
TITLE OF INVENTION: CONSTITUTIVELY TRANSLOCATING CELL LINE
FILE REFERENCE: NRK.108
CURRENT APPLICATION NUMBER: US/11/040,218
CURRENT FILING DATE: 2005-01-21
PRIOR APPLICATION NUMBER: US/10/788,197
PRIOR APPLICATION NUMBER: US/10/788,197
PRIOR APPLICATION NUMBER: PCT/US03/14581
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CURRENT APPLICATION NUMBER: US/11/040,218
CURRENT FILING DATE: 2005-01-21
PRIOR APPLICATION NUMBER: US/10/788,197
PRIOR FILING DATE: 2004-02-26
PRIOR PPLICATION NUMBER: US/10/788,197
PRIOR FILING DATE: 2003-05-12
PRIOR FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: 60/379,986
PRIOR APPLICATION NUMBER: 60/401,698
PRIOR APPLICATION NUMBER: 60/401,698
PRIOR FILING DATE: 2002-08-07
NUMBER OF SEQ ID NOS: 94
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SEQ ID NO 63
LENGTH: 388
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Best Local Similarity
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APPLICANT: HUDSON, CHRISTINE C.
TITLE OF INVENTION: CONSTITUTIVELY TRANSLOCATING
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No. US20060029983A1
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97.8%;
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Pred. No. 1.1e-175;
0; Mismatches 8;
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Length

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300 240 240 180 180 120 120 60

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APPLICANT: OMLLEY, ROBERT H.

APPLICANT: HUDSON, CHRISTINE C.

TITLE OF INVENTION: CONSTITUTIVELY TRANSLOCATING CEI

FILE REFERENCE: NRK.108

CURRENT APPLICATION NUMBER: US/11/040,218

CURRENT FILING DATE: 2005-01-21

PRIOR APPLICATION NUMBER: US/10/788,197

PRIOR FILING DATE: 2004-02-26

PRIOR FILING DATE: 2004-02-26

PRIOR FILING DATE: 2003-05-12

PRIOR APPLICATION NUMBER: 60/379,986

PRIOR APPLICATION NUMBER: 60/379,986

PRIOR APPLICATION NUMBER: 60/401,698

PRIOR APPLICATION NUMBER: 60/401,698

PRIOR FILING DATE: 2002-08-07

NUMBER OF SEQ ID NOS: 94
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US-11-040-218-67
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-040-218-65
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                                                        SOFTWARE: PatentIn Ver.
SEQ ID NO 67
LENGTH: 370
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Best Local Similarity
Matches 358; Conserv
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SEQ ID NO 65
ОКGANISM: Homo sapiens
-11-040-218-67
                    TYPE: PRT
ORGANISM: H
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PRIOR APPLICATION NUMBER: 60/401,698
PRIOR FILING DATE: 2002-08-07
NUMBER OF SEQ ID NOS: 94
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Pred. No. 1.1e-175;
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SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 69, Application US/11040218
publication No. US20060029983A1
GENERAL INFORMATION:
APPLICANT: OAKLEY, ROBERT H.
APPLICANT: HUDSON, CHRISTINE C.
APPLICANT: INVENTION: CONSTITUTIVELY TRANSLOCATING CELL LINE
FILE REFERENCE: NRK.108
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Best Local Similarity
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PRIOR APPLICATION NUMBER: PCT/US03/14581
PRIOR FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: 60/379,986
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: 60/401,698
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CURRENT FILING DATE: 2005-01-21
PRIOR APPLICATION NUMBER: US/10/788,197
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2002-08-07
                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Homo sapiens
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                                                                                                            MANYSHAADNILQNLSP--LTAFLKLTSLGFIIGVSVVGNLLISILLVKDKTLHRAPYYF
                                                                                                                                             MANTTGEPEEVSGALSPPSASAYVKLVLLGLIMCVSLAGNAILSLLVLKERALHKAPYYF
                                     LLDLCCSDILRSAICFPFVFNSVKNGSTWTYGTLTCKVIAFLGVLSCFHTAFMLFCISVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLDLCCSDILRSAICFPFVFNSVKNGSTWTYGTLTCKVIAFLGVLSCFHTAFMLFCISVT
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62.7%;
                                                                                                                                                                                    64.7%; Score 1288.5;
62.7%; Pred. No. 3.56
tive 56; Mismatches
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Pred. No. 3.4e-117;
6; Mismatches 77;
                                                                                                                                                                                                    5; DB 7;
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US-11-040-218-71
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                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                          Matches 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OAKLEY, ROBERT H.
APPLICANT: HUDSON, CHRISTIME C.
APPLICANT: HUDSON, CONSTITUTIVELY TRANSLOCATING
FILE REFERENCE: NRK.108
CURRENT APPLICATION NUMBER: US/11/040,218
CURRENT FILING DATE: 2005-01-21
                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 388
                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                               121 RYMAIAHHRFYAKRMTLWTCAAVICMAWTLSVAMAFPPVFDVGTYKFIREEDQCIFEHRY 180
||:|||||||||||:||
|| RYLAIAHHRFYTKRLTFWTCLAVICMVWTLSVAMAFPPVLDVGTYSFIREEDQCTFQHRS 178
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                                    239
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                                                                                                                                                                                                 61 LLDLCLADGIRSAVCEPEVLASVRHGSSWTFSALSCKIVAFMAVLFCFHAAFMLFCISVT
                                                                                                                                                                                                                                                  1 MANTTGEPEEVSGALSPPSASAYVKLVLLGLIMCVSLAGNAILSLLVLKERALHKAPYYF
                                                                                                                                                                                                                           SPYIVACYWRVEVKACAVPHRYLATAVWNSFAQAAVNPIVCELLNKDLKKCL-TTHAPCW
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                                                AAANWIAGFGRGPMPPTLLGIRQNGHAAS-RRLLGMDEVKGEKQLGRMFYAITLLFLLIW
                                                                                  FKANDTLGFMLMLAVLMAATHAVYGKLLLFBYRHRKMKPVQMVPAISQNWTFHGPGATGQ
                                                                                                                                                                               LLDLCCSDILRSAICFPFVFNSVKNGSTWTYGTLTCKVIAFLGVLSCFHTAFMLFCISVT
                                    AAANWLAGFGRGPTPPTLLGIRONANTTGRRRLLVLDEFKMEKRISRMFYIMTFLFLTLW
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                                                                                                                                                                                                                                                                                     63.6%;
                                                                                                                                                                                                                                                                         ; Score 1266; DB 7;
; Pred. No. 5.4e-115;
54; Mismatches 80;
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    US-11-165-024-3
; Sequence 3, Application US/11165024
; Dublication No. US20050266527A1
; GENERAL INFORMATION:
; APPLICANT: Li et al.
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; TYPE: PRT; ORGANISM: Homo sapiens US-11-040-218-73
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US-11-040-218-73
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PRIOR APPLICATION NUMBER: PCT/US03/14581
PRIOR FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: 60/379,986
PRIOR APPLICATION NUMBER: 60/379,986
PRIOR FILING DATE: 2002-05-13
PRIOR FILING DATE: 2002-06-07
NUMBER OF SEQ ID NOS: 94
PRIOR FILING DATE: 2002-08-07
NUMBER OF SEQ ID NOS: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. SEQ ID NO 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 73, Application US/11040218 Publication No. US20060029983A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 63.6%;
Best Local Similarity 62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 230;
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CURRENT FILING DATE: 2005-01-21
PRIOR APPLICATION NUMBER: US/10/788,197
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APPLICANT: HUDSON, CHRISTINE C.
TITLE OF INVENTION: CONSTITUTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: NRK.108
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                                        359 GTGGAPAP
                                                                                                     300 SPYIVACYWRVEVKACAVPHRYLATAVWMSFAQAAVNDIVCFLLNKDLKKCL-TTHAPCW 358
                                                                                                                                                              253
                                                                                                                                                                                       15 MANYSHAADNILQNLSP--LTAFLKLTSLGFIIGVSVVGNLLISILLVKDKTLHRAPYYF
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                                                                              GPYLVACYWRVFARGPVVPGGFLTAAVWMSFAQAGINPFVCIFSNRBLRRCFSTTLLYCA
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                                                                                                                                                                                                                                                                                                                            RYLAIAHHRFYTKRLTFWTCLAVICMVWTLSVAMAFPPVLDVGTYSFIREEDQCTFQHRS
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AARGRTPP
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  380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1266; DB 7;
Pred. No. 5.6e-115;
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293

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CURRENT APPLICATION NUMBER: US/11/165,024
CCURRENT FILING DATE: 2005-06-24
PRIOR APPLICATION NUMBER: US 10/006,394
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: US 09/228,420
PRIOR APPLICATION NUMBER: US 08/465,971
PRIOR APPLICATION NUMBER: US 08/465,971
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VETBION 3.3
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-10-995-561-901
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                                                                                                                                                                                                                                                               APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE,
TITLE OF INVENTION: DETECTION AND USES THEREOF
PILE REFERENCE: CL001559
CURRENT FAPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 901, Application US/10995561 Publication No. US20050272054A1 GENERAL INFORMATION:
                                                                              Matches
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Best Local :
                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                         ORGANISM: Homo sapiens -10-995-561-901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 350
TYPE: PRT
ORGANISM: Homo Bapiens
                                                                                                                                                                                                                       LENGTH: 471
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLLFLLLWSPYIVACYWRVFVKACAVPHRYLATAVWMSFAQAAVNPIVCFLLNKDLKK 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I FEHRY FKANDTLGFMLMLAVLMAATHAVYGKLLLFEYRHRKMKPVQMVPAISQNWTFHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASWNGTEAPGGGARATPYSLQVTLTLVCLAGLLMLLTVFGNVLVIIAVFTSRALKAPQNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLVSLASADILVATLVIPFSLANEVMG-YWYFGKAWCEIYLALDVLFCTSSIVHLCAISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDOKWYVISSCIGSFFAPCLIMI---LVYVRIYQIAKRRTRVPPSR-----RG
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                                                                           Conservative
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                                                                                             12.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---APPG--GLQGRGRSASGLPRRRAGAGGQNREKRFTFVLAVV 279
                                                                         63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63; Mismatches 166;
                                                                                                  Score 257; DB 6; Length 471; Pred. No. 3.1e-17;
                                                                           Mismatches
                                                                           155;
                                                                         Indels
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US-10-875-716-10
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Publication No. US20050266522A1
GENERAL INFORMATION:
APPLICANT: Li et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/988,745
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US 09/314,006
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: US 08/467,559
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 10
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CURRENT FILING DATE: 2004-06-25
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                  128 HRFYAKRMTLWTCAAVICMAWTLSVAMAFPPVFDVGTYKFIREEDQCIFEHRYFKANDTL
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                                                     GFGRGPMPPTLLGIRQNGHA----
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                                                                                                                                                                                                     TRYSSKRRV----TVMISIVWVLSFTISCPLLFGLNN----ADQNECIIANPAFVVYSSI 186
                                                                                                     ---VSFYVPFIVTLLVYIKIYIVLRRRKKVNTK---RSSRAFRAHLRAPLKEAARR----
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       --EKNGHAKDHPKIAKIFEIQTMPNGKTRTSLKTMSRRKLSQQK---E
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US-11-090-439-16
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US-10-875-716-9
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                                           Sequence 9, Application US/10875716
Publication No. US20050266522A1
GENERAL INFORMATION:
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Best Local
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TITLE OF INVENTION: Immortalized Human Tuberous Sclerosis Null
TITLE OF INVENTION: Angiomyolipoma Cell and Method of Use Ther
FILE REFERENCE: 24318-502
CURRENT APPLICATION NUMBER: US/11/090,439
CURRENT FILING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: 60/556,344
PRIOR FILING DATE: 2004-03-25
APPLICANT: Li et al. TITLE OF INVENTION: Human Amine Receptor FILE REFERENCE: PF188D1C2
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ORGANISM: Homo sapiens
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23.5%; Pred. No. 3.4e-15;
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CURRENT APPLICATION NUMBER: US/10/875,716
CURRENT FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 09/988,745
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: US 09/314,006
PRIOR FILING DATE: 1999-05-19
PRIOR PRIOR DATE: 1999-05-06
PRIOR PILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 9
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                                                                                                                                            TITLE OF INVENTION: Methods, Compositions and TITLE OF INVENTION: Amyloid-Beta Protein Protein Protein Reference: P27,800-B USA
CURRENT APPLICATION NUMBER: US11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR FILING DATE: 2004-08-24
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
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; ORGANISM: Homo sapiens US-11-127-877-51
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                                                 SOFTWARE: PatentIn version 3.3
SEQ ID NO 51
LENGTH: 429
TYPE: PRT
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Best Local Similarity
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APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Laenen, Wendy
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 ASADLVMGLLVVPFGATIVVWG-RWEYGSFFCELWTSVDVL-CVTASIETLCVIALDRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 ALSPPSASAYVKL------VLIGLIMCVSLAGNAILSLLVLKERALHKAPYYFLLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLADGIRSAVCFPFVLASVRHGSSWTFSALSCKIVAFMAVLFCFHAAFMLFC-ISVTRYM 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIF--EHRYFKANDTLGFMLMLAVLMAATHAVYGKLLLFEYRHRKMKPVQMVPAISQNWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AITSPFRYQSLLTRARARALVCTVWAISALVSFLPIL---MHWWRAESDEARRCYNDPKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIAHHREYAKRMTLWTCAAVICMAWTLSVAMAEPEVEDVGTYKEIREEDQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLLPPASEGSAPLSQQWTAGMGLLVALIVLLIVVGNVLVIVAIAKTPRLQTLTNLFIMSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLLNKDLKK-----CLTTHAPC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKTLG----IIMGVFTLCWLPFFLANVVKAFHRD-LVPDRLFVFFNWLGYANSAFNPII-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FHGPGATGQAAANWIAGFGR-----GPMPPTLLGIRQNGHAASR----RLLGMDEVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDFVTNRAYAIASSVVSFYVPLCIM-----AFVYLRVFREAQKQVKKID------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SCERRFLGGPARPPSPEPSPSPGPPRPADSLANGRSSKRRPSRLVALREQKA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 231; DB 6; I
; Pred. No. 7.6e-15;
64; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                         and Compound Assays For Inhibiting Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280
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|  | Qy 112 FMLFCISVTRYMAIAHHRFYAKRMTLWTCAAVICMAWTLSVAMAFPPVFDVGTYKF | Qy 57 PYYFILDLCLADGIRSAVCFPFVLASVRHGSSWTFSALSCKIVAFMAVLFCFHAA | Qy 1 MANTTGEPEEVSGALSPPSASAYVKLVLLGLIMCVSLAGNAILSLLVLKERALHKA | Query Match 11.1%; Score 220.5; DB 7; Length 466; Best Local Similarity 21.0%; Pred. No. 1e-13; Matches 88; Conservative 61; Mismatches 162; Indels 109; Ga | RESULT 15 US-11-127-877-50 US-11-127-877-50 US-11-127-877-50  (**) Publication No. US20050287565A1 (**) Publication No. US20050287565A1 (**) REPLICANT: Morchiers, Pascal G. APPLICANT: Morchiers, Pascal G. APPLICANT: Hoffmann, Marcel APPLICANT: Spittaels, Koenraad F. F. APPLICANT: Laenen, Wendy (**) TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting TITLE OF INVENTION: Amyloid-Beta Protein Production FILE REFERENCE: P27,800-8 USA CURRENT APPLICATION NUMBER: US/11/127,877 CURRENT APPLICATION NUMBER: 60/570,352 PRIOR APPLICATION NUMBER: 60/570,352 PRIOR FILING DATE: 2004-08-12 PRIOR APPLICATION NUMBER: 60/603,948 PRIOR FILING DATE: 2004-08-24 NUMBER OF SEQ ID NOS: 590 SOPTWARE: Patentin version 3.3 SEQ ID NO 50 LENGTH: 466 TYPE: PRT CORGANISM: Homo sapiens | Db 310 IVFWLGYLNSCINPIIYPCSSQEFKKAFQNVLRIQCLRRKQSSKHALGYTLHPPSQAVEG | Qy 324 TAVWMSFAQAAVNPIVCFLLNKDLKKCLTHAPCWGTGG | VVGCEVLCWLPFE | QY 264 NGHAASRRLLGMDEVKGEKQLGRMFYAITLLELLLMSPYIVACYWRVFVKACAVPHRYLA | 227 SDSEQVTLR | Qy 214 +HRKMKPVQMVPAISQNWTFHGPGATGQAAANWIAGFGRGPMPPTLLGIRQ | QY 172 DQCIFEHRYFKANDTLGEMLMLAVLMAATHAVYGKLLLFEYR | 115 MGLCIISIDRYIGVSYPLRYPTIVTQ | 112 PMLECISVTRYMAIAHHREYAKRMTLWTCAAVICMAWTLSVAMAEDPVEDVGT | Db 61 THYYIVNLAVADLLLTSTVLPESAIFEVLGYMAFGRVFCNIMAAVDVLCCTAS | SVRH | 1 MVFLSGNASDSSNCTQPPAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSV | QY 1 MANTTGEPEEVSGALSPPSASAYVKLVLLGLIMCVSLAGNAILSLLVLKERALHKA | Query Match 11.1%; Score 220.5; DB 7; Length 429;<br>Best Local Similarity 21.0%; Pred. No. 9.5e-14;<br>Matches 88; Conservative 61; Mismatches 162; Indels 109; Gaps |
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